

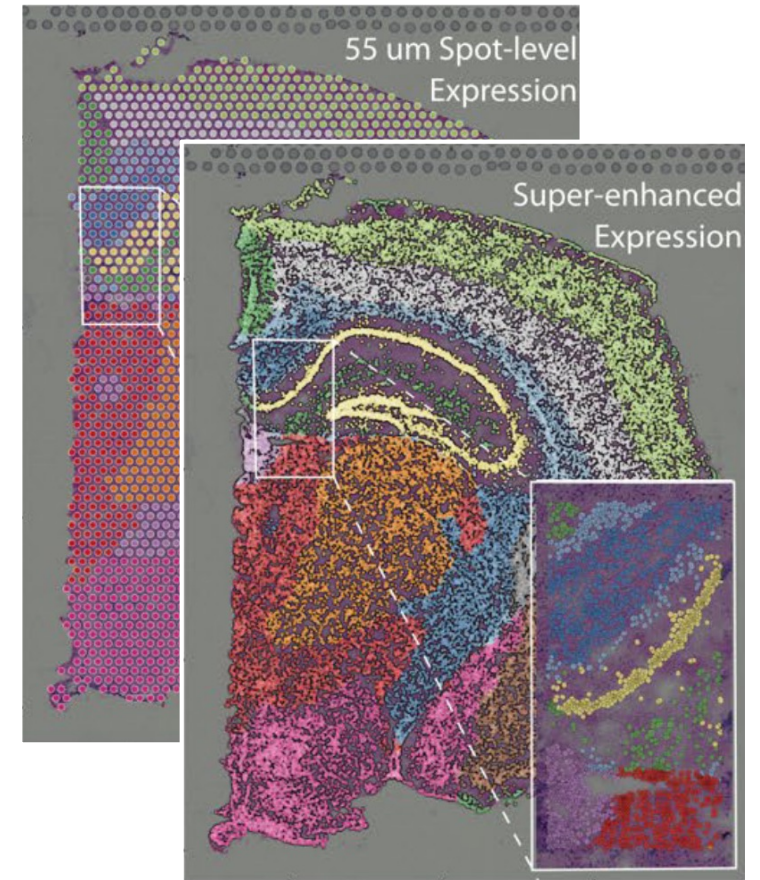
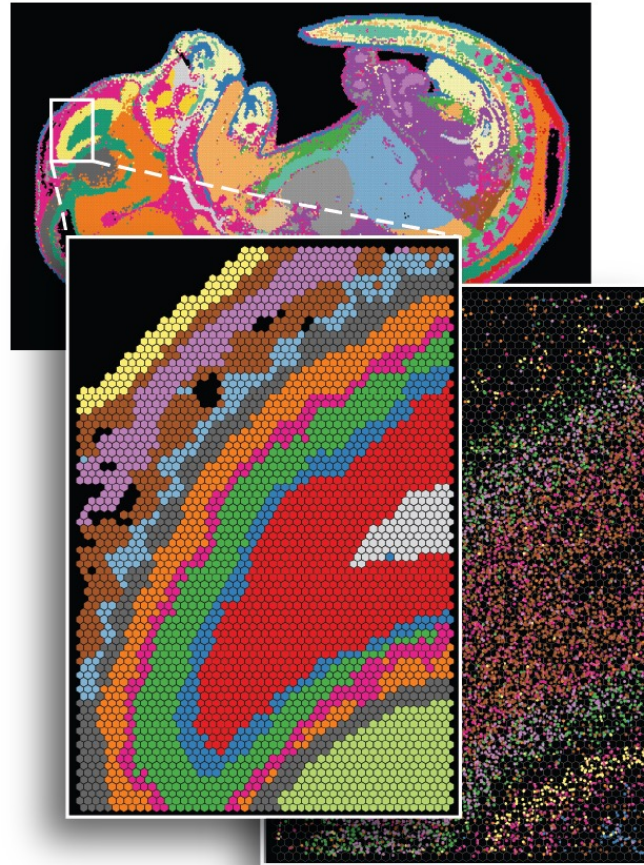
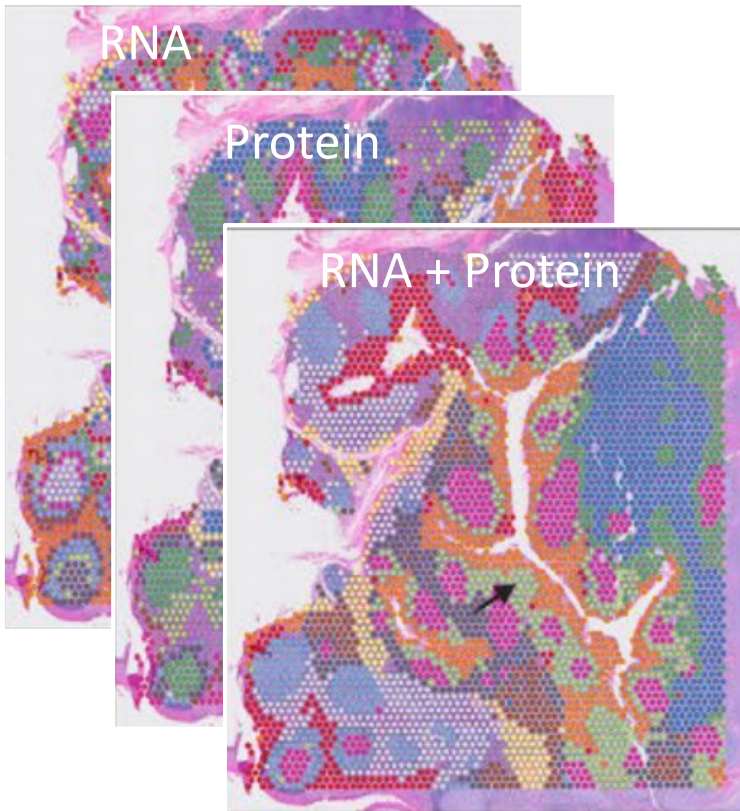
Giotto Suite: a spatial multi-scale and multi-omics analysis framework

Ruben Dries, Assistant Professor of Medicine

- Department of Medicine
 - Hematology & Oncology
 - Computational Biomedicine
- Department of Bioinformatics
- www.drieslab.com

Spatial Multi-Omics Workshop
02/12/2024

Spatial multi-omics data analysis



Spatial multi-omics data analysis

Giotto Suite: a multi-scale and technology-agnostic spatial multi-omics analysis framework



Giotto Suite



Giotto Suite is a major upgrade to the Giotto package that provides tools to process, analyze and visualize **spatial multi-omics data at all scales and multiple resolutions**. The underlying framework is generalizable to virtually all current and emerging spatial technologies. Our Giotto Suite prototype pipeline is generally applicable on various different datasets, such as those created by state-of-the-art spatial technologies, including *in situ* hybridization (seqFISH+, merFISH, osmFISH, CosMx), sequencing (Slide-seq, Visium, STARmap, Seq-Scope, Stereo-Seq) and imaging-based multiplexing/proteomics (CyCIF, MIBI, CODEX). These technologies differ in terms of resolution (subcellular, single cell or multiple cells), spatial dimension (2D vs 3D), molecular modality (protein, RNA, DNA, ...), and throughput (number of cells and analytes).

Installation

To install Giotto suite use `devtools::install_github("drieslab/Giotto")`.

Visit the Giotto [Discussions](#) page for more information.

Website Update!

With Giotto version 4.0, we updated the website at <http://giottosuite.com>, you can still find the previous website at <https://giottosuite.readthedocs.io/en/latest/>

Website description

- **Get started:** Here you can find more advanced information about the Giotto object, Giotto ecosystem, Giotto configuration, and installation FAQs.
- **Documentation:** Here you will find all Giotto functions grouped by their purpose (Helpers, Getters & Setters, Visualization, ...)
- **Examples:** Here you can find end-to-end examples for different technologies and datasets.
- **Tutorials:** Here you can find various tutorials on working with Giotto (analysis, visualizations, working on the cloud, ...)
- **News:** Here you can find the changelog for every Giotto release and video recordings from previous presentations.

Links

[Browse source code](#)

[Report a bug](#)

License

[Full license](#)

GPL (>= 3)

Community

[Contributing guide](#)

[Code of conduct](#)

Citation

[Citing Giotto](#)

Developers

[Ruben Dries](#)

Author, maintainer

[Jiaji George Chen](#)

Author

[Joselyn C. Chávez-Fuentes](#)

Author

[Guo-Cheng Yuan](#)

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[Matthew O'Brien](#)

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[Edward Ruiz](#)

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[Wen Wang](#)

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[Natalie Del Rossi](#)

Author

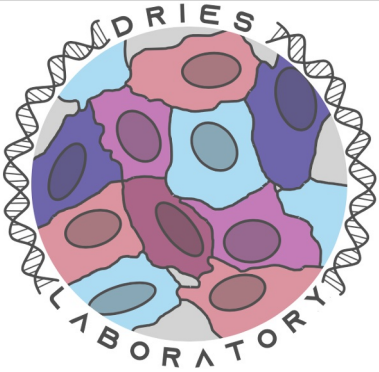
For users:

- **Examples:** vignettes for different datasets and technologies
- **Tutorials:** what can you do in or with Giotto?
- **News page** for regular updates

For developers:

- **Giotto Ecosystem** and sub-websites
- **Giotto Class Structure** to understand data structures
- **Contribution page**

Acknowledgements: Giotto Suite work



Jiaji (George) Chen
Graduate Student



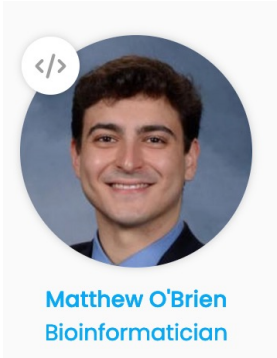
Yuan Laboratory



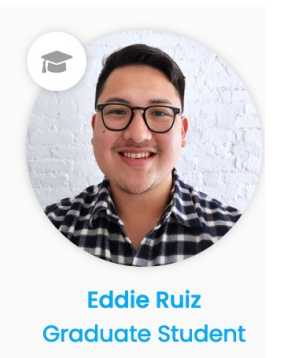
Joselyn Chávez

Wen Wang
Pratishtha Guckhool
Adriana Sistig
Natalie Del Rossi

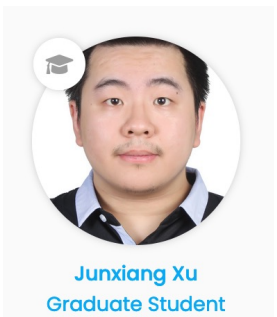
Funding:



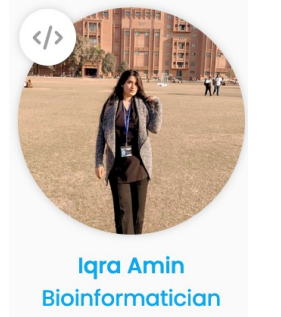
Matthew O'Brien
Bioinformatician



Eddie Ruiz
Graduate Student



Junxiang Xu
Graduate Student



Iqra Amin
Bioinformatician

Bringing computation to biology by bridging the last mile

Anne E. Carpenter & Shantanu Singh

 Check for updates

“Usable tools are the ‘last mile’ bridge between what computer science makes possible and what biologists are able to put to widespread use in their research.”

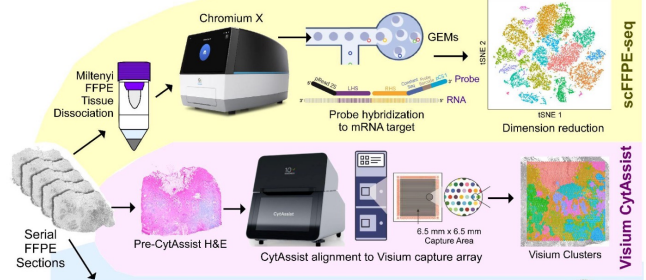
Why Giotto Suite?

- ❑ There are many spatial technologies, we need **technology-agnostic** structures.
- ❑ The number of datasets and methods exponentially increase, it's **now or never**
- ❑ Spatial omics data is **complex**, and requires more complex data structures

Next generation datasets

High resolution mapping of the breast cancer tumor microenvironment using integrated single cell, spatial and in situ analysis of FFPE tissue

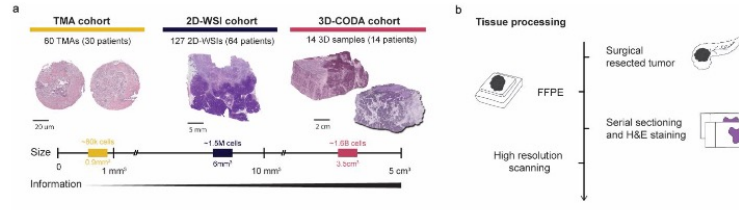
Amanda Janesick, Robert Shelansky, Andrew D. Gottscho, Florian Wagner, Morgane Rouault, Ghezal Beliakoff, Michelli Faria de Oliveira, Andrew Kohlway, Jawad Arousoud, Carolyn A. Morrison, Tingsheng Yu Drennon, Seayar H. Mohabbat, Stephen R. Williams, 10x Development Teams, Sarah E.B. Taylor



Three-dimensional assessments are necessary to determine the true, spatially-resolved composition of tissues

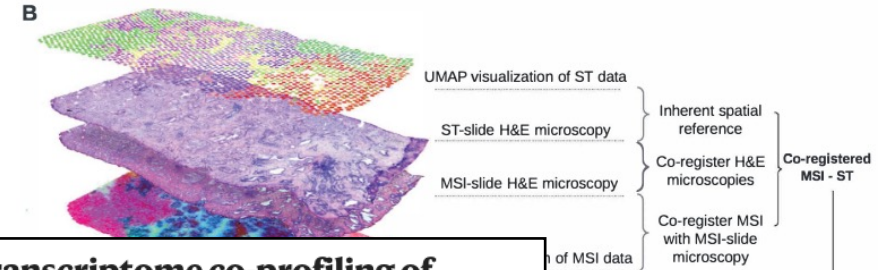
André Forjaz, Eduarda Vaz, Valentina Matos Romero, Saurabh Joshi, Alicia M. Braxton, Ann C. Jiang, Kohei Fujikura, Toby Cornish, Seung-Mo Hong, Ralph H. Hruban, Pei-Hsun Wu, Laura D. Wood, Ashley L. Kiemen, Denis Wirtz

doi: <https://doi.org/10.1101/2023.12.04.569986>



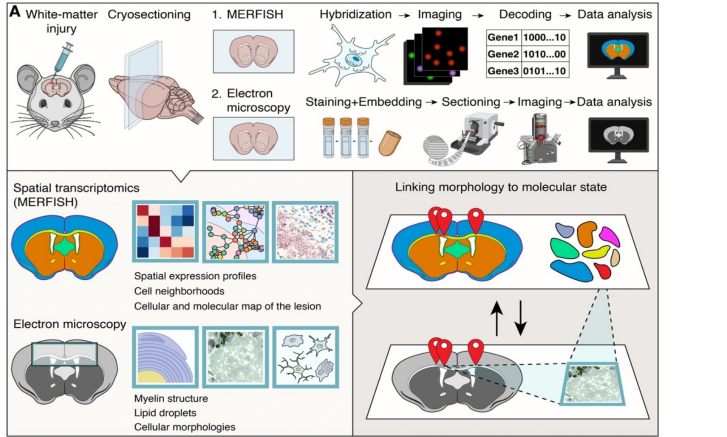
Integration of Multiple Spatial Omics Modalities Reveals Unique Insights into Molecular Heterogeneity of Prostate Cancer

Wanqiu Zhang, Xander Spotbeen, Sebastiaan Vanuytven, Sam Kint, Tassiani Sarretto, Fabio Socciairelli, Katy Vandereyken, Jonas Dehaïrs, Jakub Idkowiak, David Wouters, Jose Ignacio Alvira Larizgoitia, Gabriele Partel, Alice Ly, Vincent de Laat, Maria José Q Mantas, Thomas Gevaert, Wout Devlies, Chui Yan Mah, Lisa M Butler, Massimo Loda, Steven Joniau, Bart De Moor, Alejandro Sifrim, Shane R. Ellis, Thierry Voet, Marc Claesen, Nico Verbeeck, Johannes V. Swinnen



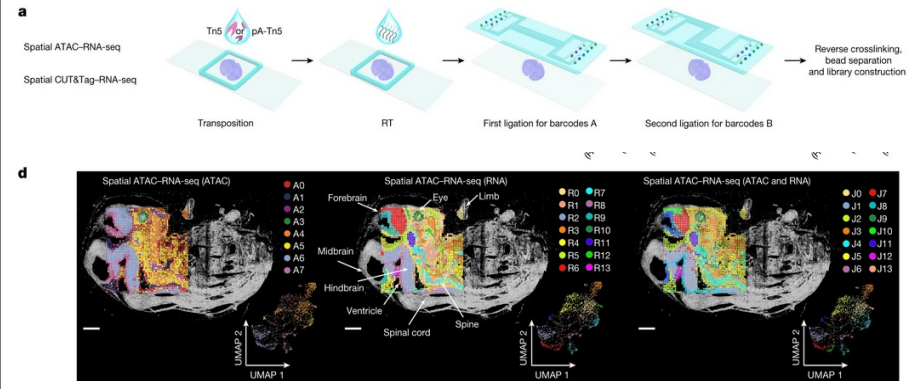
Spatial Transcriptomics-correlated Electron Microscopy maps transcriptional and ultrastructural responses to brain injury

Peter Androvic, Martina Schifferer, Katrin Perez Anderson, Ludovico Cantuti-Castelvetri, Hany Jiang, Hao Ji, Lu Liu, Garyfallia Gouna, Stefan A. Berghoff, Simon Besson-Girard, Johanna Knoferle, Mikael Simons & Ozgun Gokce



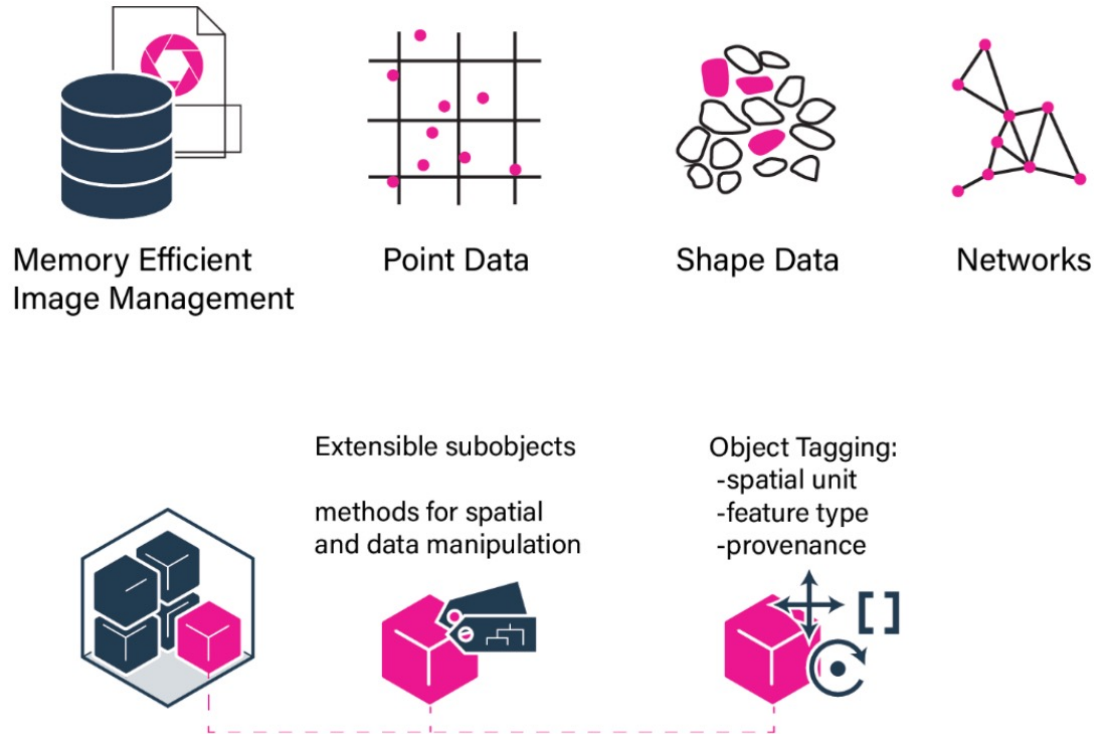
Spatial epigenome-transcriptome co-profiling of mammalian tissues

Di Zhang, Yanxiang Deng, Petra Kukanja, Eneritz Agirre, Marek Bartosovic, Mingze Dong, Cong Ma, Sai Ma, Graham Su, Shuozen Bao, Yang Liu, Yang Xiao, Gorazd B. Rosoklija, Andrew J. Dwork, J. John Mann, Kam W. Leong, Maura Boldrini, Liya Wang, Maximilian Haeussler, Benjamin J. Raphael, Yuval Kluger, Gonçalo Castelo-Branco & Rong Fan

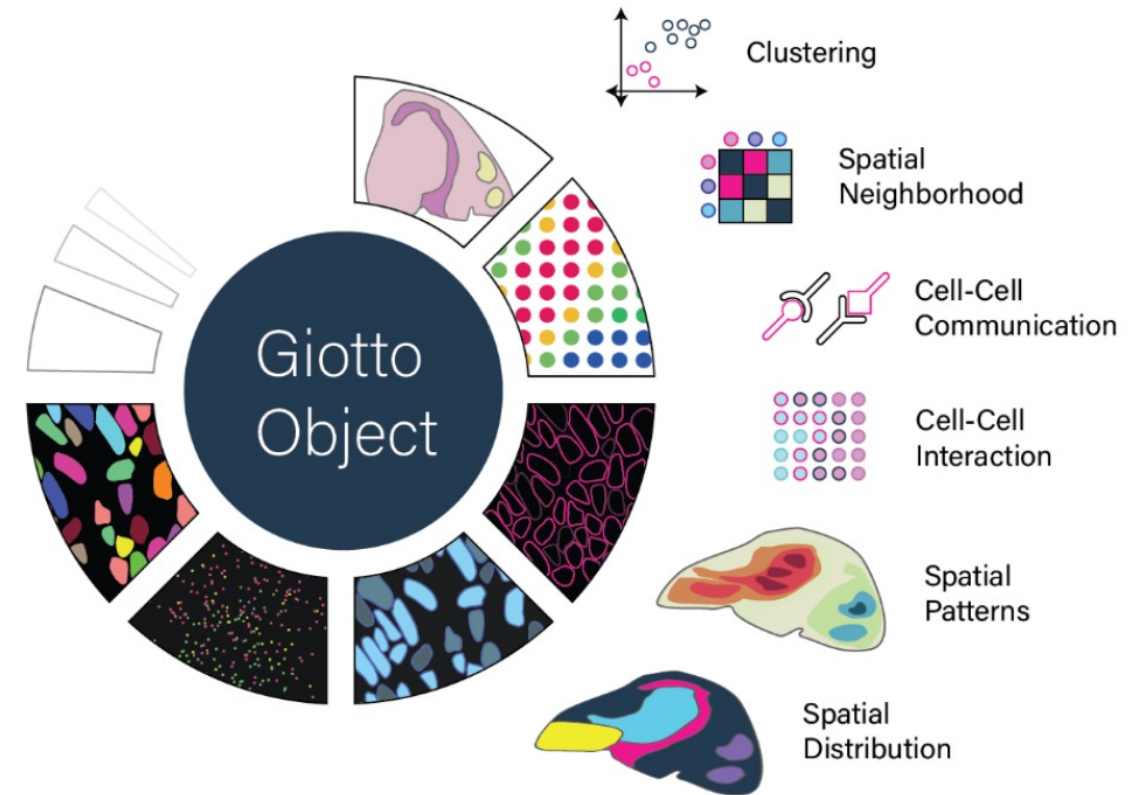


Software engineering to support next generation spatial data analysis

Innovative software engineering



Flexible and scalable spatial data analysis



Spatial omics biology at multiple scales

Technology

Spatial-Array Sequencing



Multiplexed Mass-Spec



Multiplexed Imaging

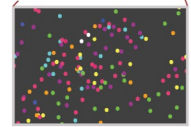
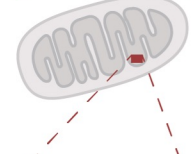
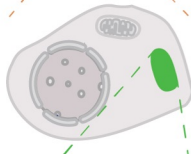
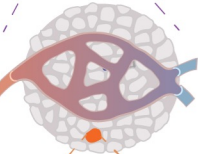
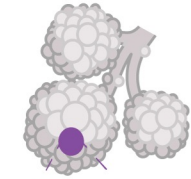


Biology

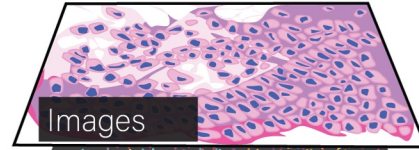
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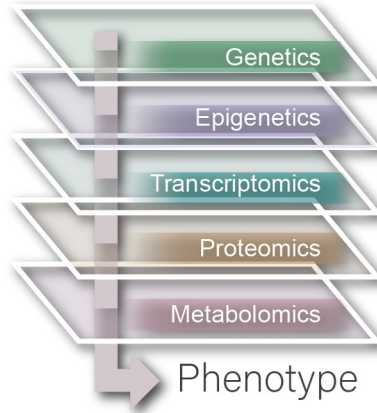


Representation



Multi-Modal

Vertically Integrated Connectome



DBiT-seq (AtlasXomics),
Visium (10X Genomics),
Slide-seq (Curio Bioscience)

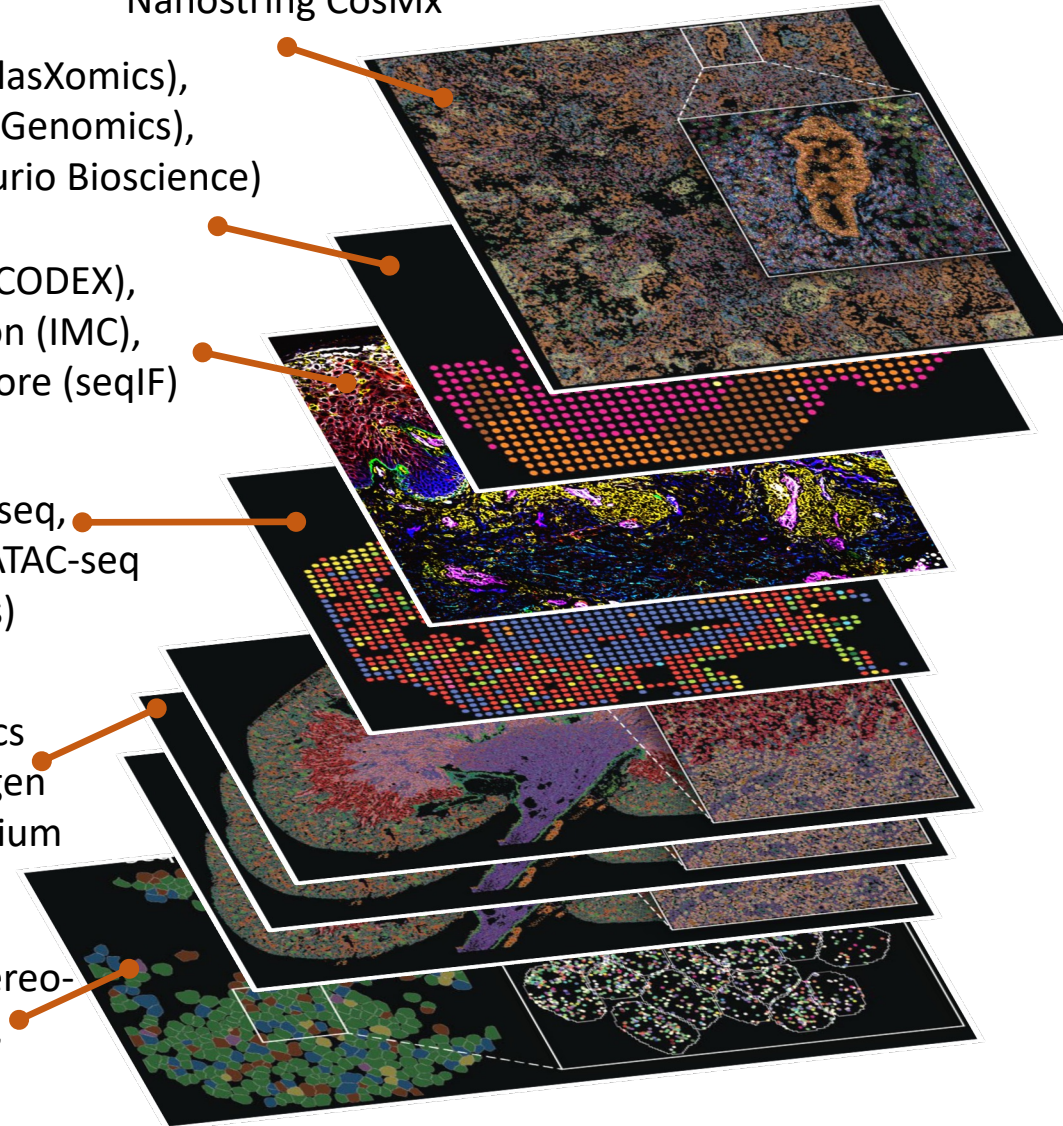
Akoya (CODEX),
Hyperion (IMC),
Lunaphore (seqIF)

Spatial CITE-seq,
CUT&RUN, ATAC-seq
(AtlasXomics)

Spatial Genomics
(seqFISH+), Vizgen
(MERFISH), Xenium
(10X Genomics)

Seq-Scope, stereo-
seq (STOmics),
Open-ST

Nanostring CosMx

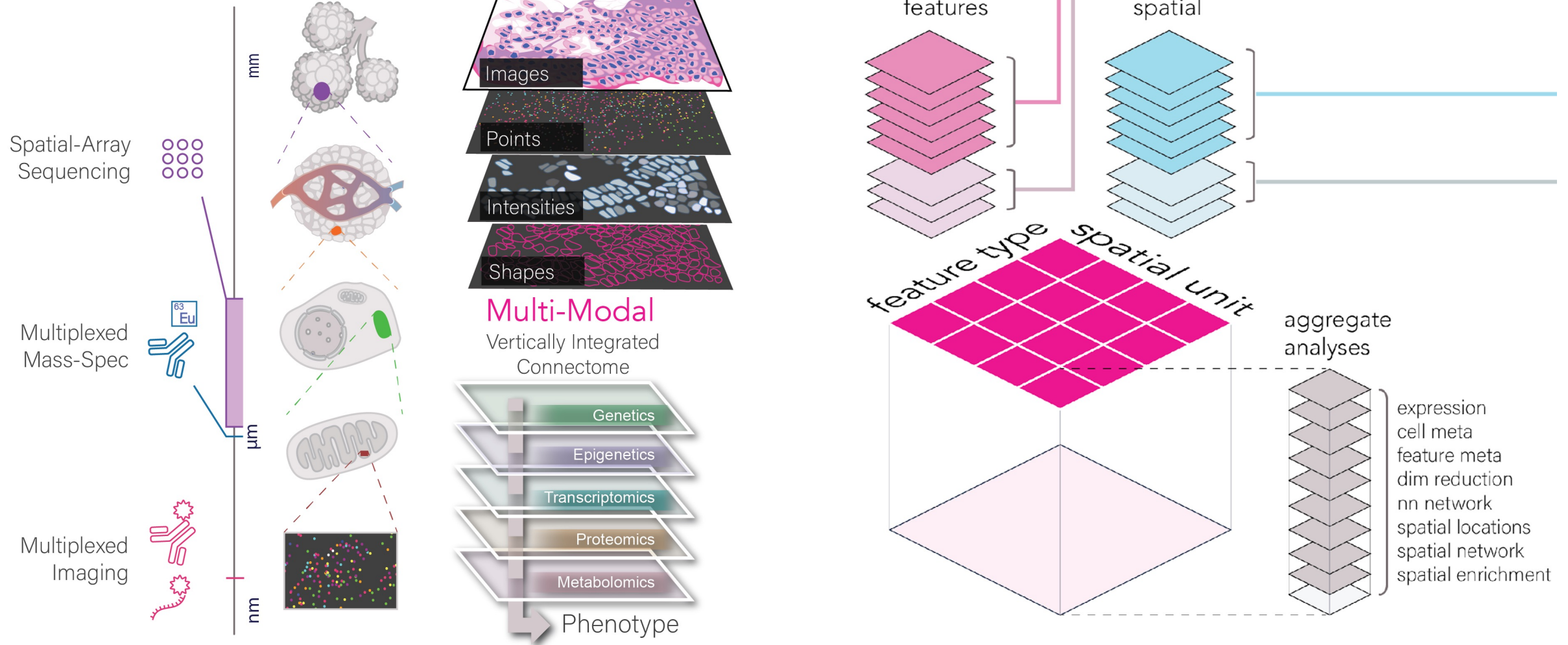


Representations for all type of data at multiple scales

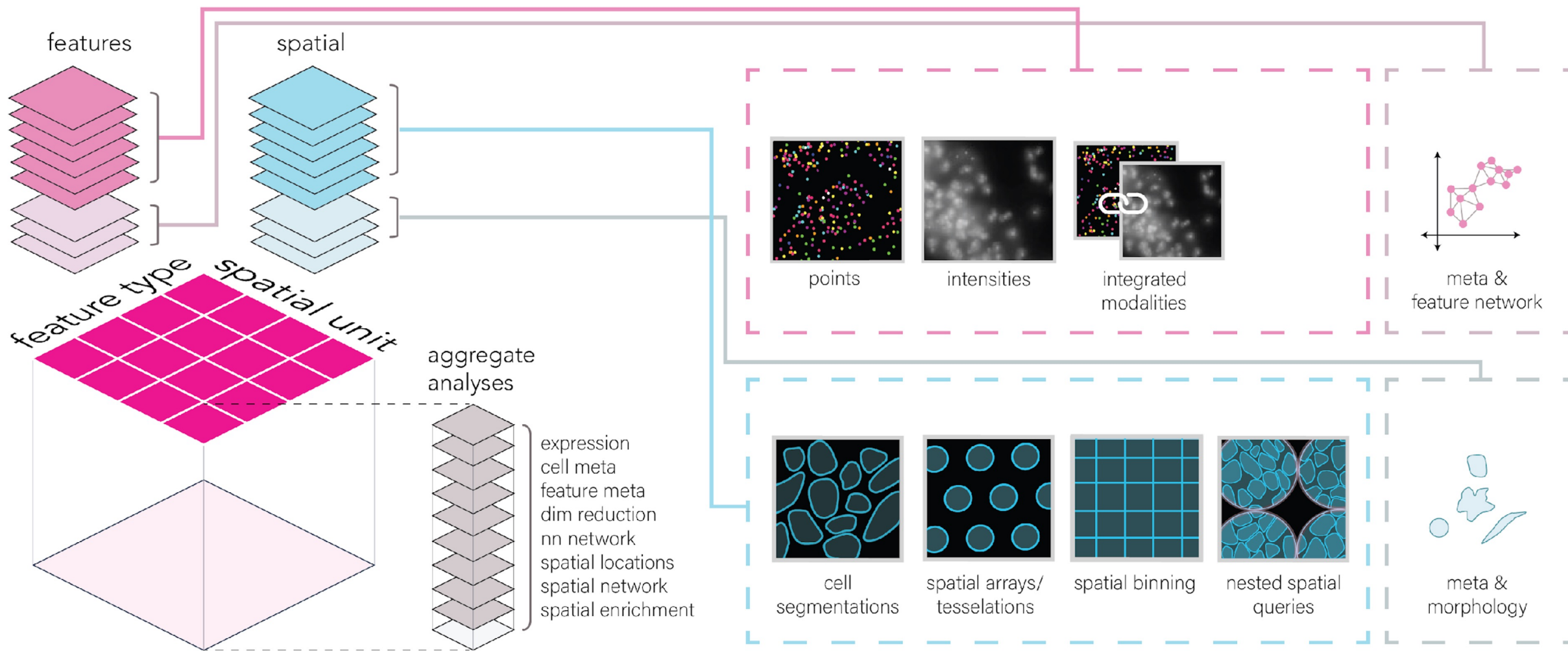
Technology

Biology

Representation

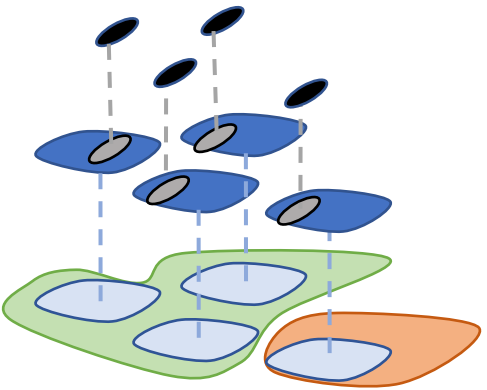


Representations for all type of data at multiple scales



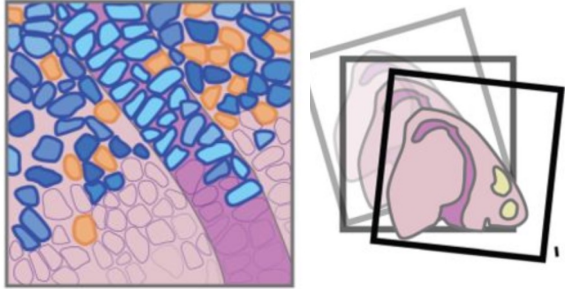
Tutorials & challenges:

Multi-scale



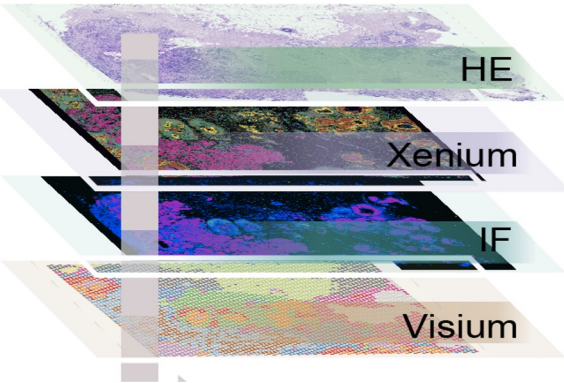
A diagram illustrating multi-scale analysis. At the bottom, a large green cell contains several smaller blue cells. Above it, several individual blue cells are shown at a higher magnification, with dashed lines connecting them to the corresponding cells in the larger cell below, representing a zoomed-in view of a specific region.

Registration & segmentation



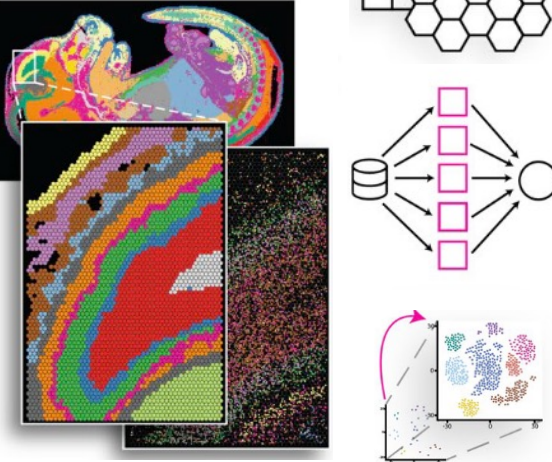
A diagram illustrating registration and segmentation. On the left, a histological image of tissue is shown with blue and orange regions. On the right, a corresponding anatomical map of a brain slice is shown, with a black box indicating a region of interest that is being registered to the histological image.

Multi-modal



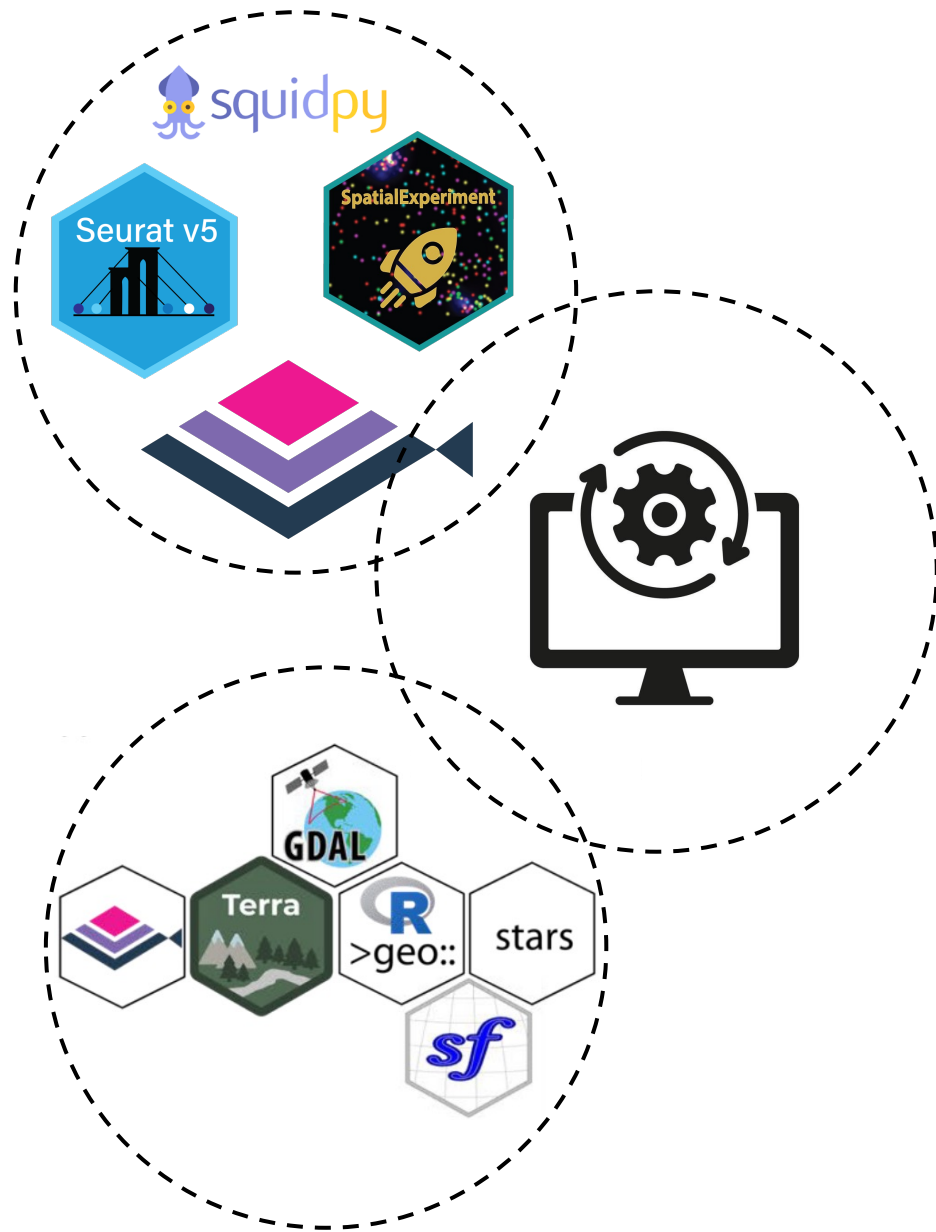
A diagram illustrating multi-modal data integration. It shows four stacked layers of data: HE (Histology), Xenium (Spatial Transcriptomics), IF (Immunofluorescence), and Visium (Spatial Transcriptomics). A vertical grey bar indicates a region of interest that is being analyzed across all four modalities.

Scalability



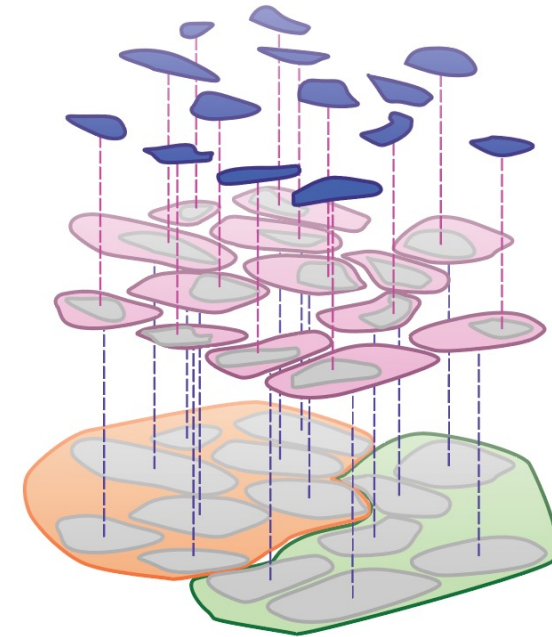
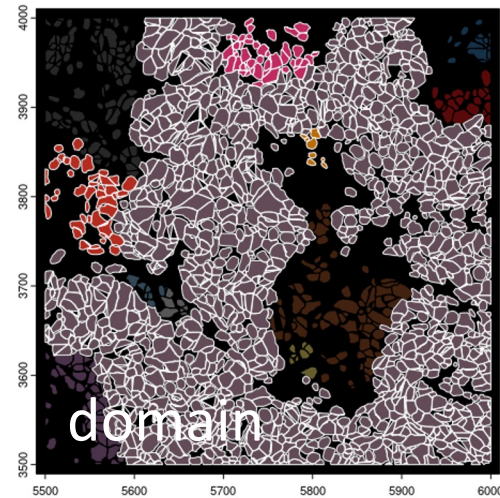
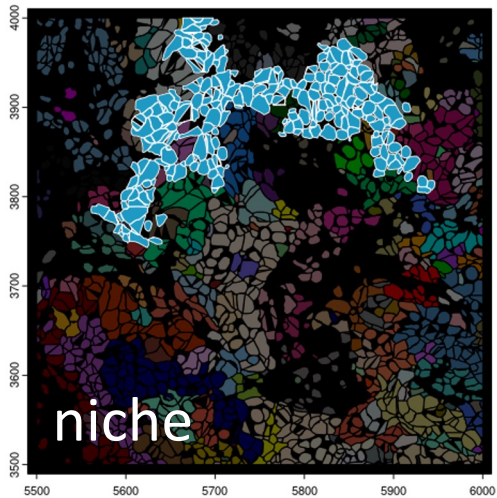
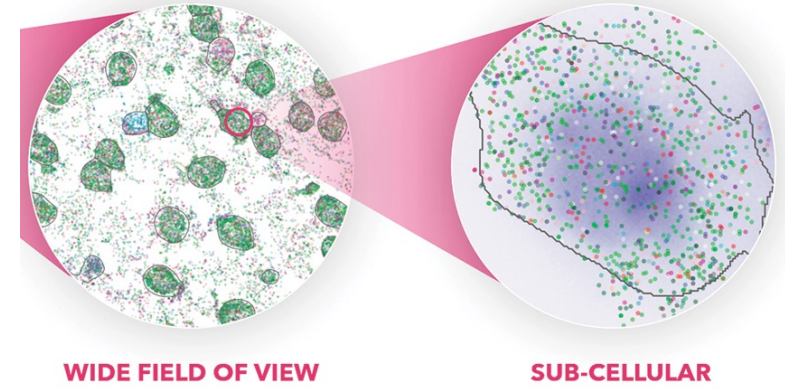
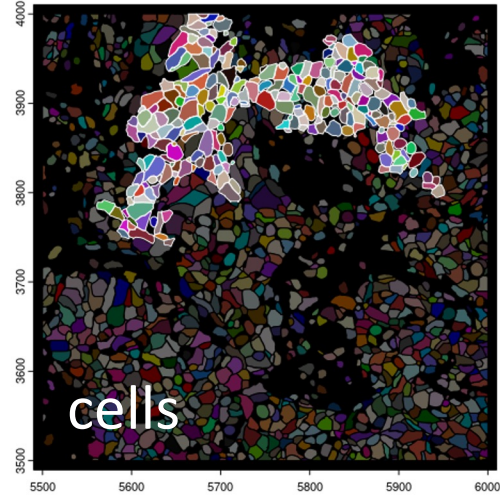
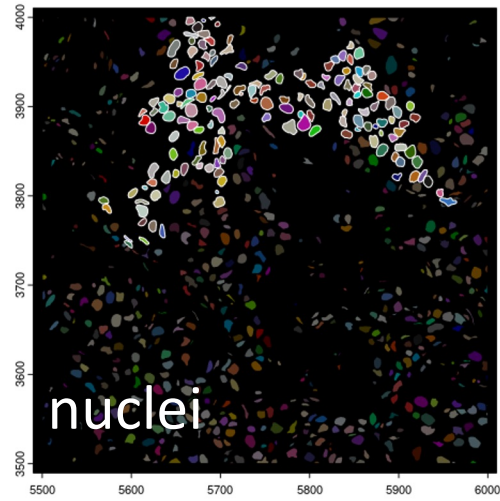
A diagram illustrating scalability challenges and solutions. On the left, a large, colorful spatial transcriptomics map is shown. On the right, a grid of cells is shown, with a zoomed-in view of a single cell. Below the grid, a diagram shows a database icon connected to a vertical stack of pink boxes, representing a data pipeline or storage system. At the bottom right, a small map shows a region of interest being analyzed.

Community & tool building:

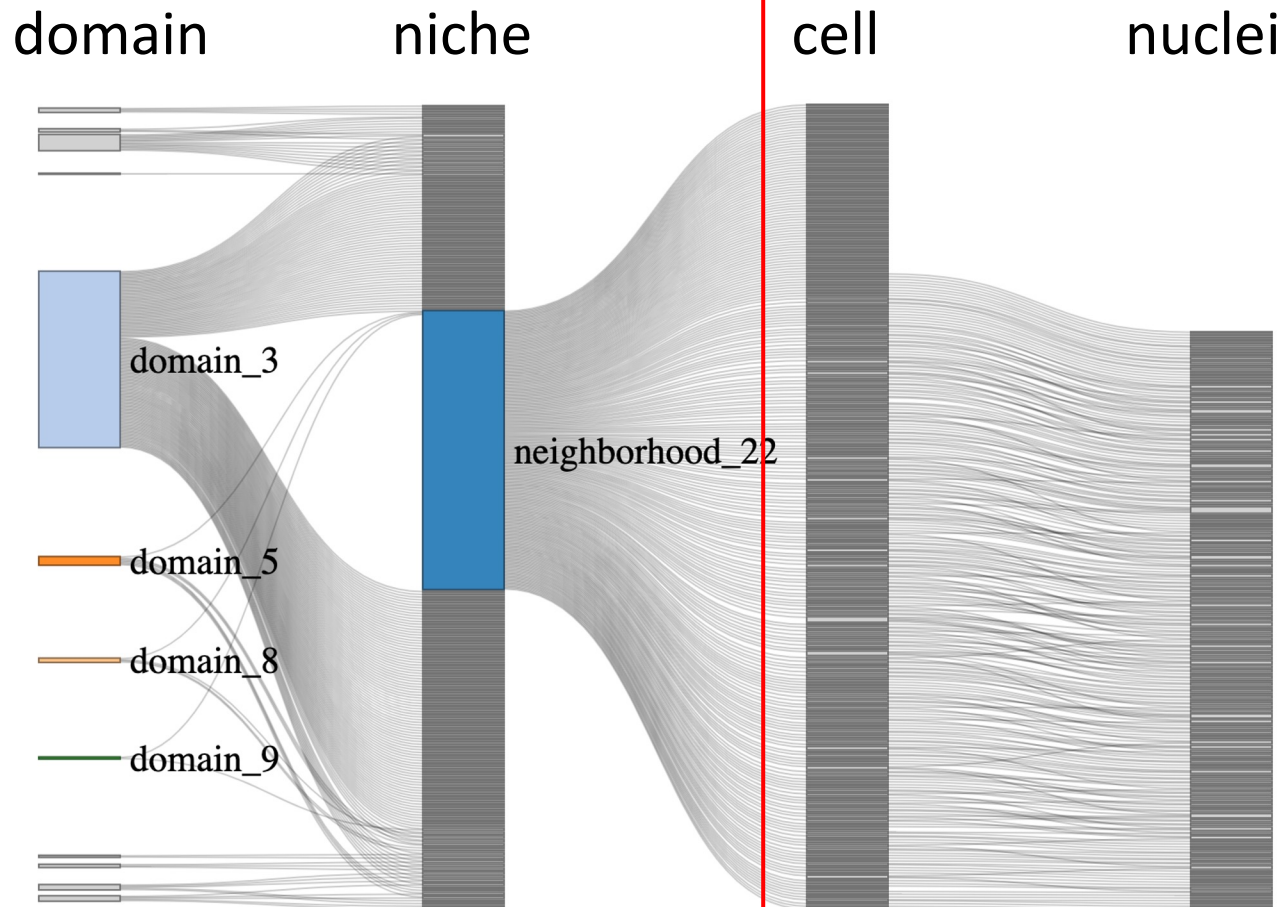
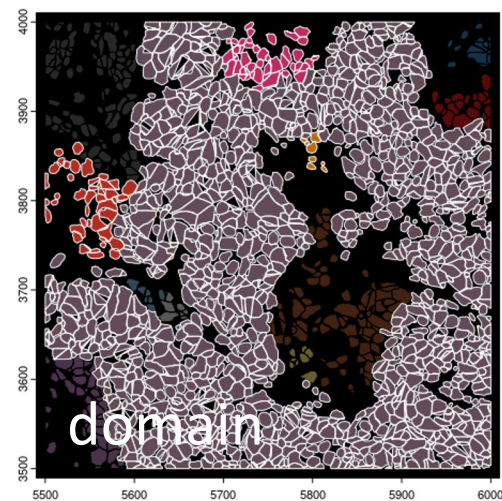
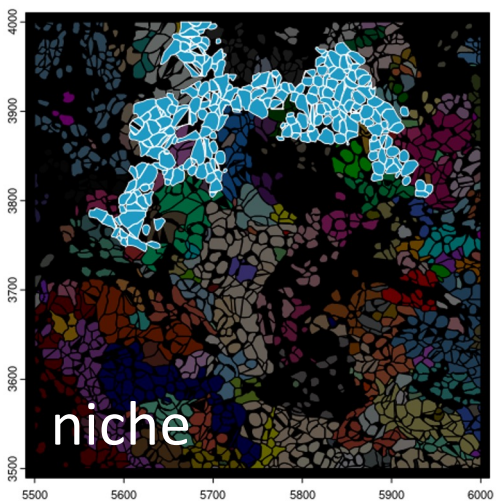
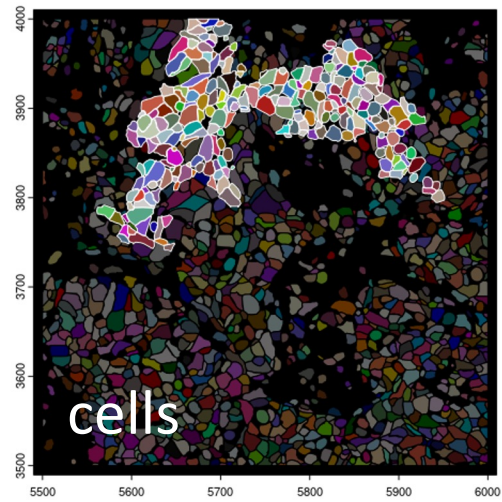
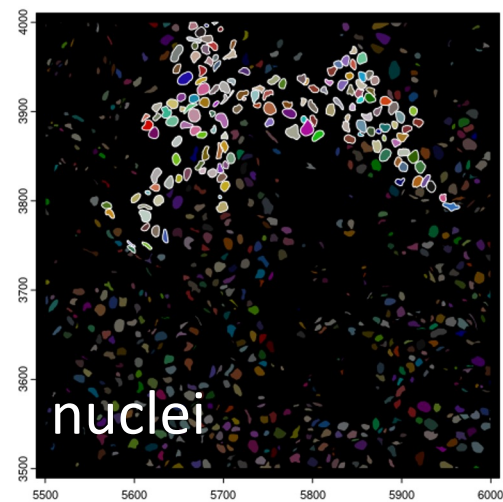


A diagram illustrating community and tool building. It features a central computer monitor icon with a gear and a circular arrow, representing a workflow or tool. Surrounding this are several circular nodes containing logos for various tools and communities: squidpy, Seurat v5, SpatialExperiment, Terra, GDAL, >geo::, stars, and sf. A large, stylized logo consisting of a pink and blue diamond shape is also present in the center.

A simple multi-scale analysis

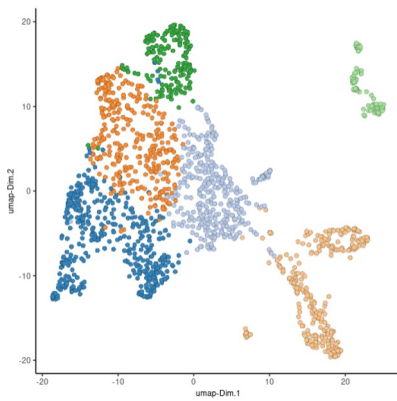
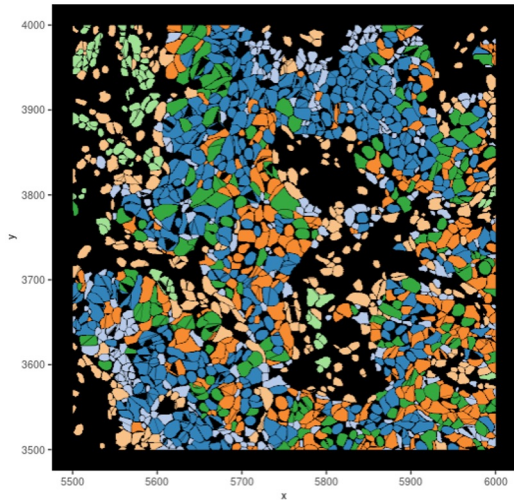
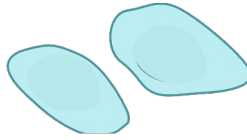


A simple multi-scale analysis

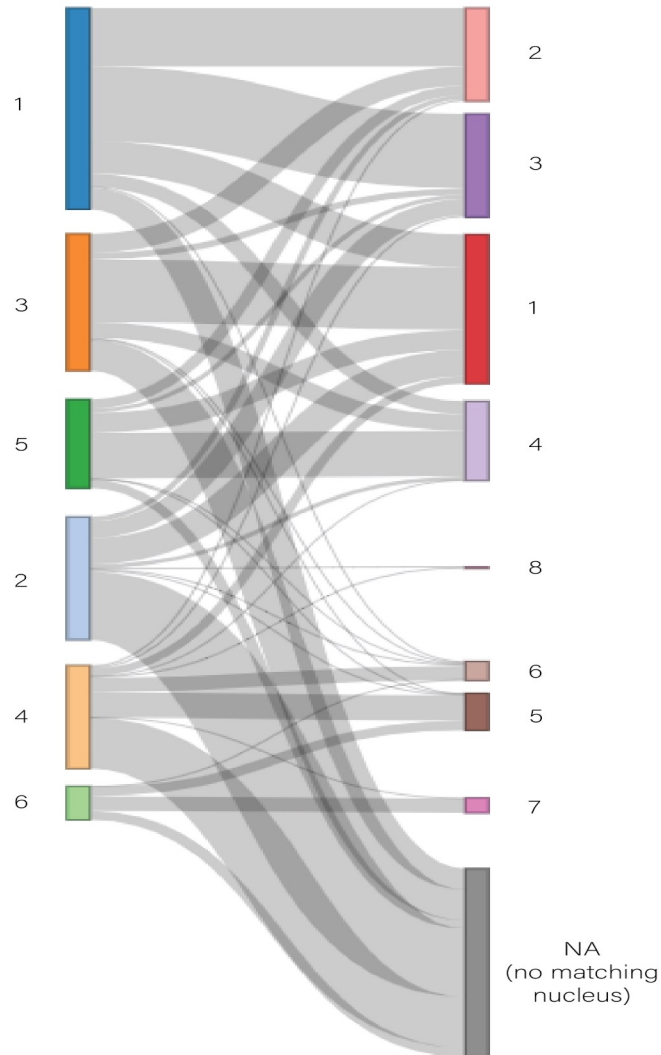
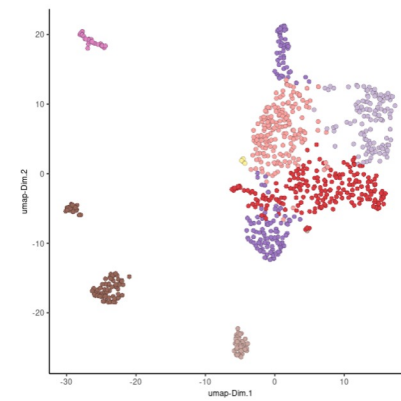
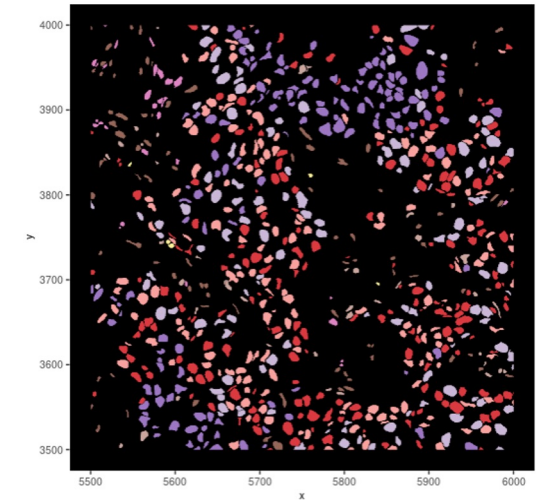
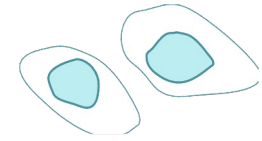


Spatial in-silico single-cell vs single-nucleus analysis

Whole cell



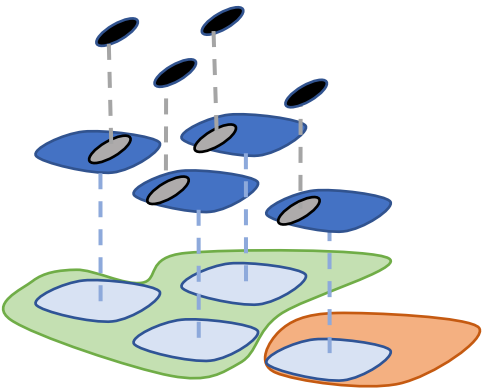
nuclei



Cell and nuclear state do not necessarily match 1-to-1

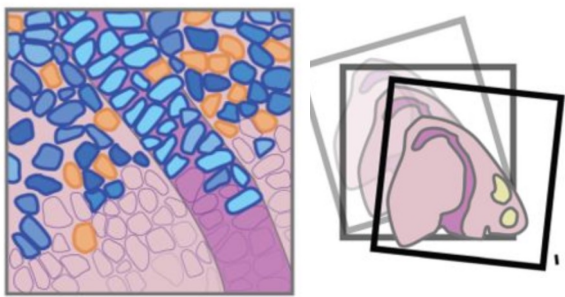
Tutorials & challenges:

Multi-scale



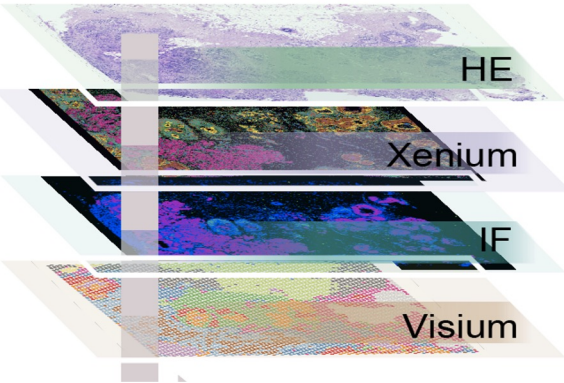
A diagram illustrating multi-scale analysis. At the bottom, a large green cell contains several smaller blue cells. Above it, several individual blue cells are shown at a higher magnification, with dashed lines connecting them to the corresponding cells in the larger cell below, representing a zoomed-in view of a specific region.

Registration & segmentation



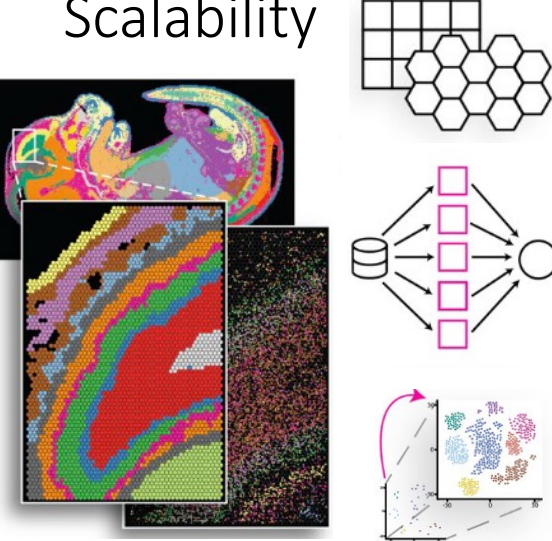
A diagram illustrating registration and segmentation. On the left is a histology slide with blue and orange cells. On the right is a segmented brain slice with a pink region highlighted. A black frame is shown overlapping the histology slide, indicating the process of aligning different data sources.

Multi-modal



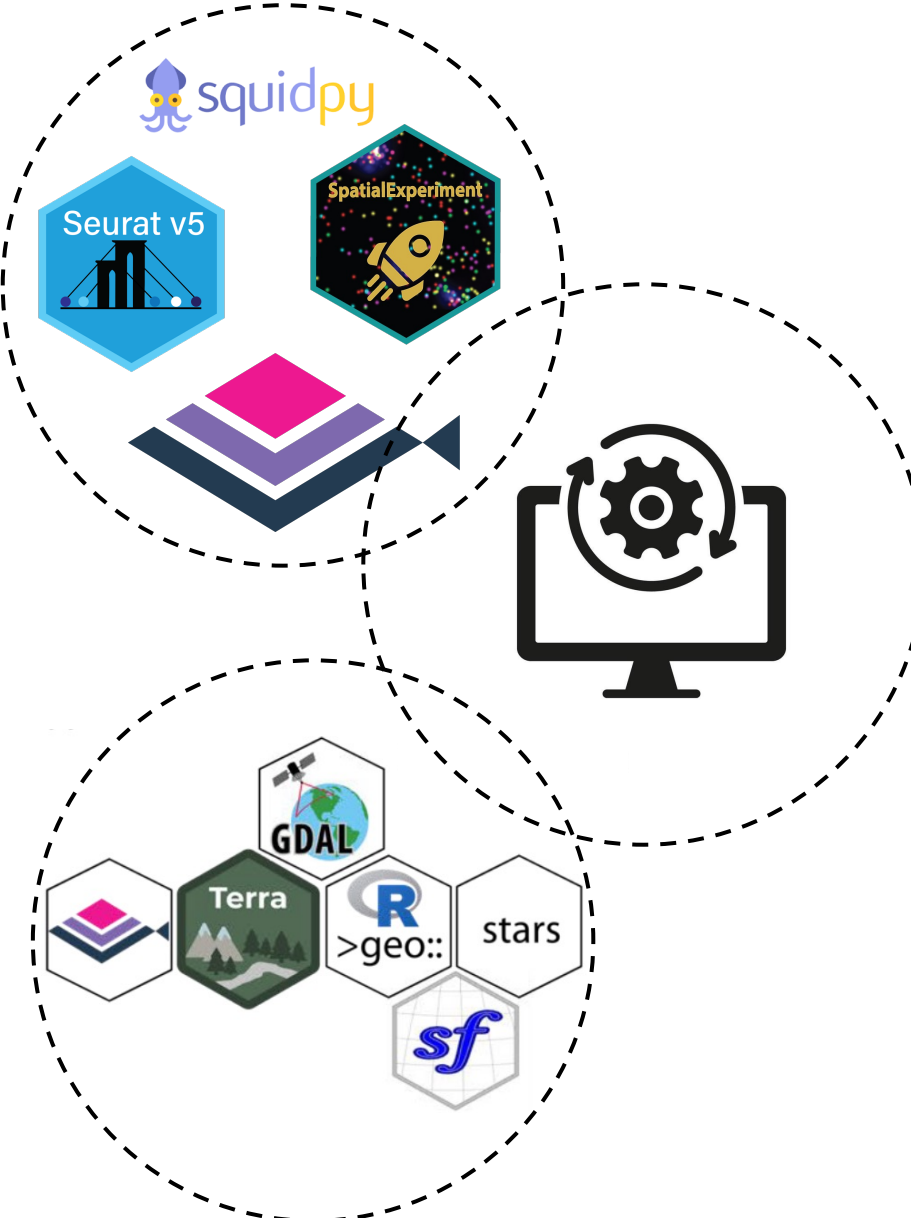
A diagram illustrating multi-modal data. It shows four stacked layers representing different data modalities: HE (Histology), Xenium (Spatially Resolved Transcriptomics), IF (Immunofluorescence), and Visium (Spatial Transcriptomics). Each layer is shown as a different colored plane with a grid overlay, indicating the spatial relationship between the different data types.

Scalability



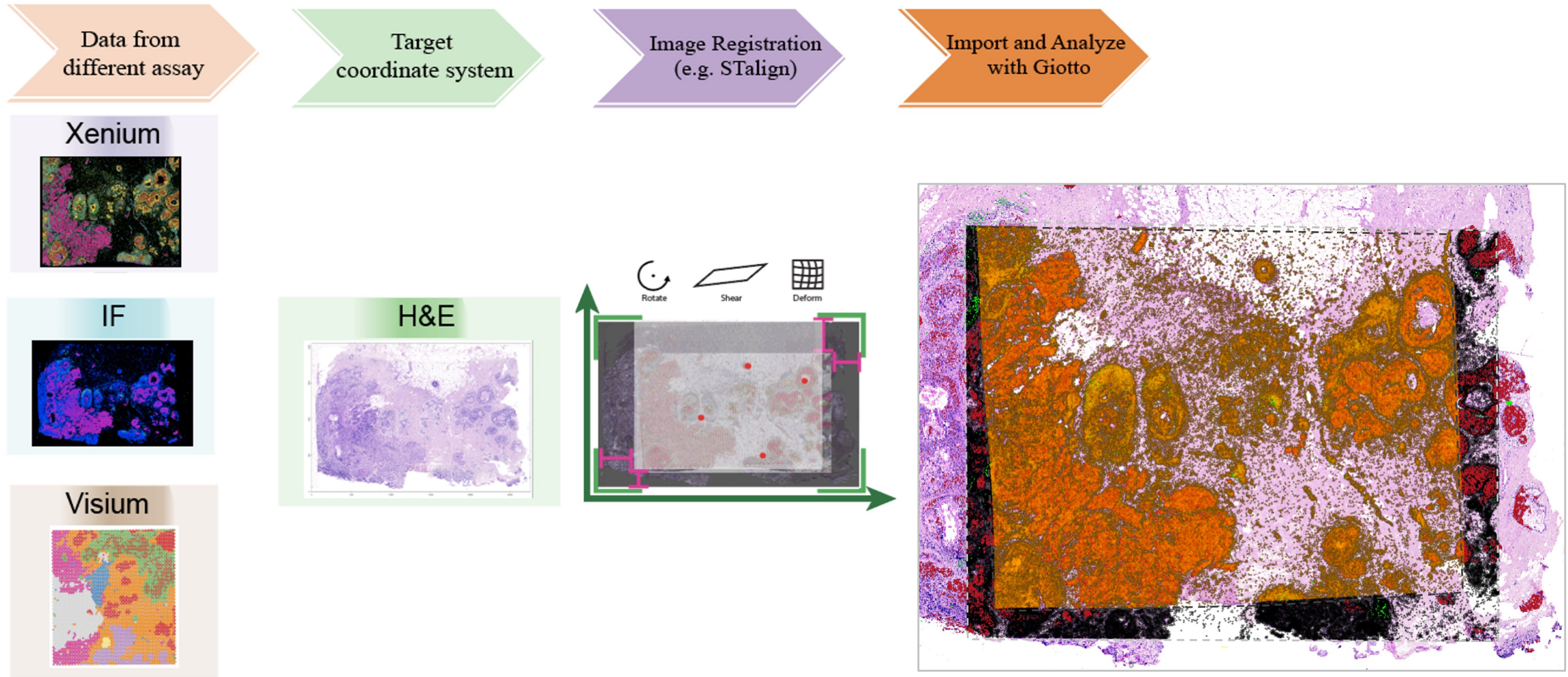
A diagram illustrating scalability. It shows a grid of cells, a neural network diagram with a database icon, and a large data visualization showing a complex spatial pattern. The neural network diagram consists of a stack of pink boxes connected by arrows, with a database icon on the left and a node on the right.

Community & tool building:



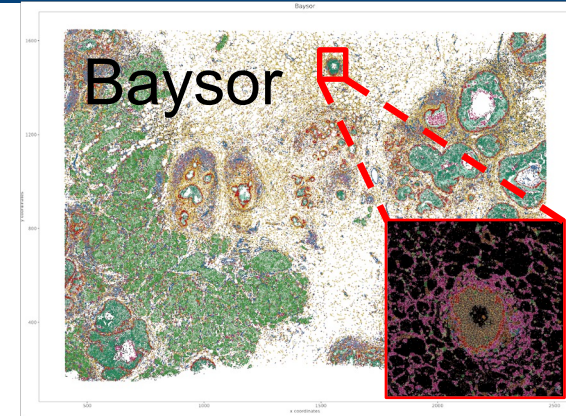
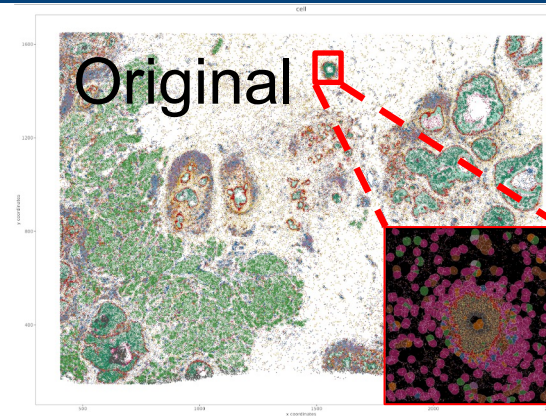
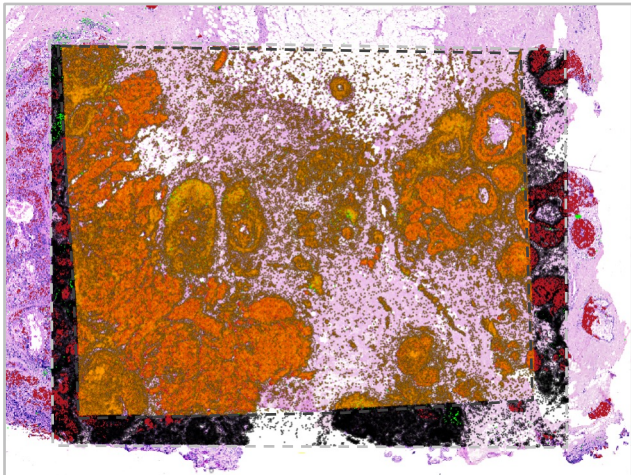
A diagram illustrating community and tool building. It features a central computer icon with a gear and a circular arrow, surrounded by various software tools and frameworks. The tools are arranged in two overlapping circles. The top circle includes squidpy, Seurat v5, and SpatialExperiment. The bottom circle includes GDAL, Terra, R, >geo::, stars, and sf. A central stack of colored layers is also visible between the two circles.

Co-registering and multi-modal data analysis

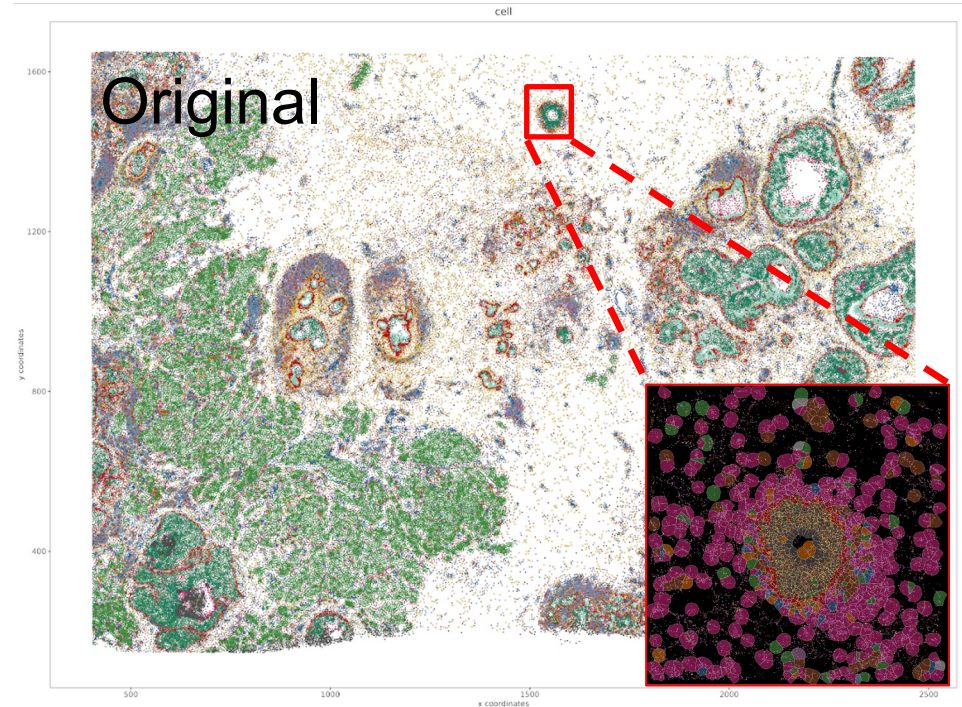
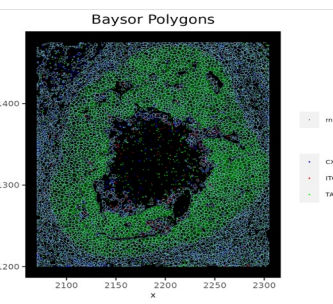
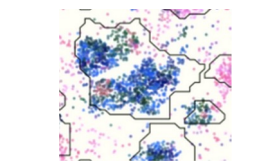
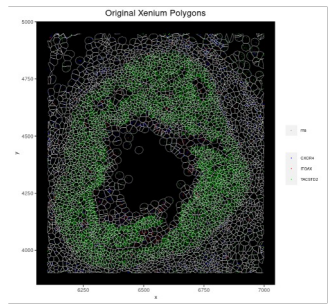
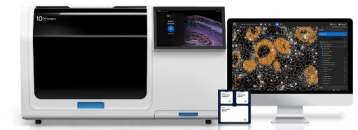


Co-registering and benchmarking cell segmentation effects

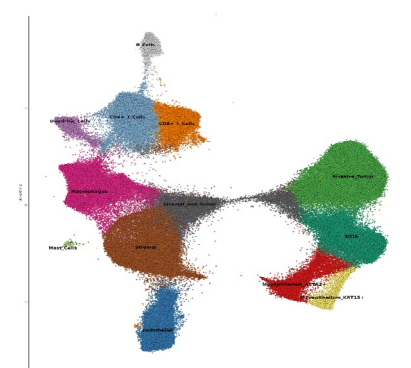
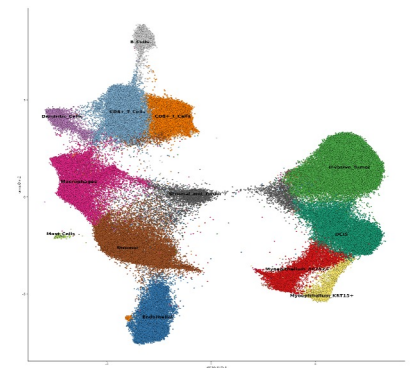
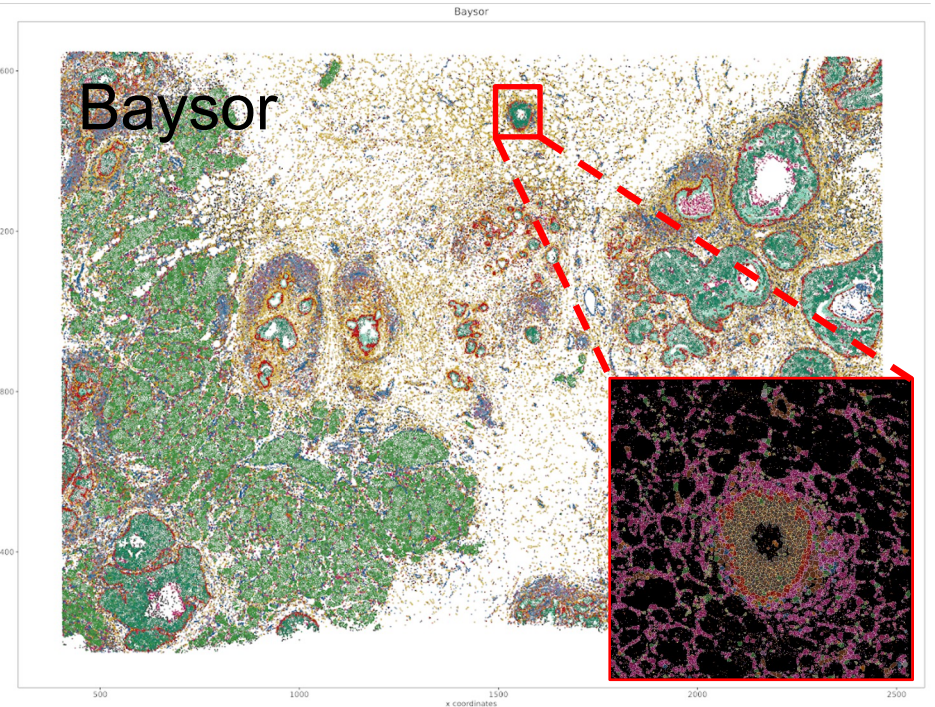
1. compare segmentation methods:



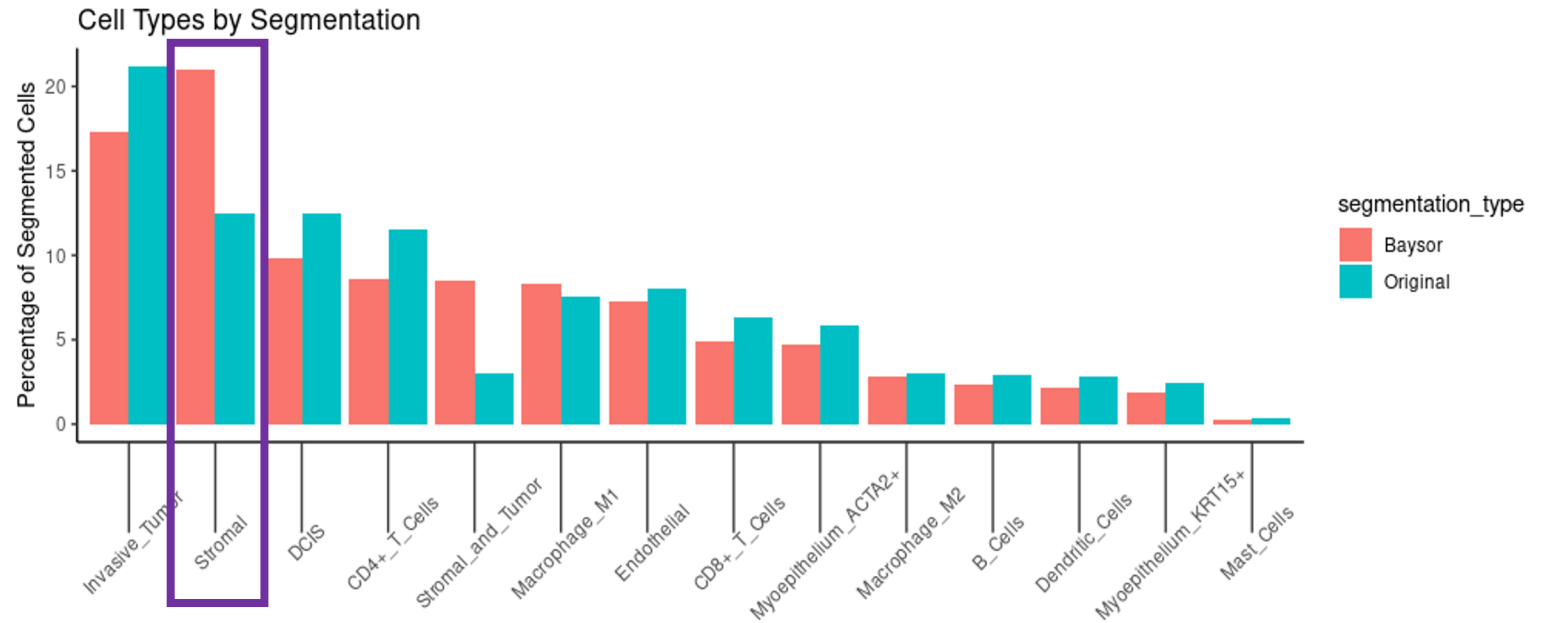
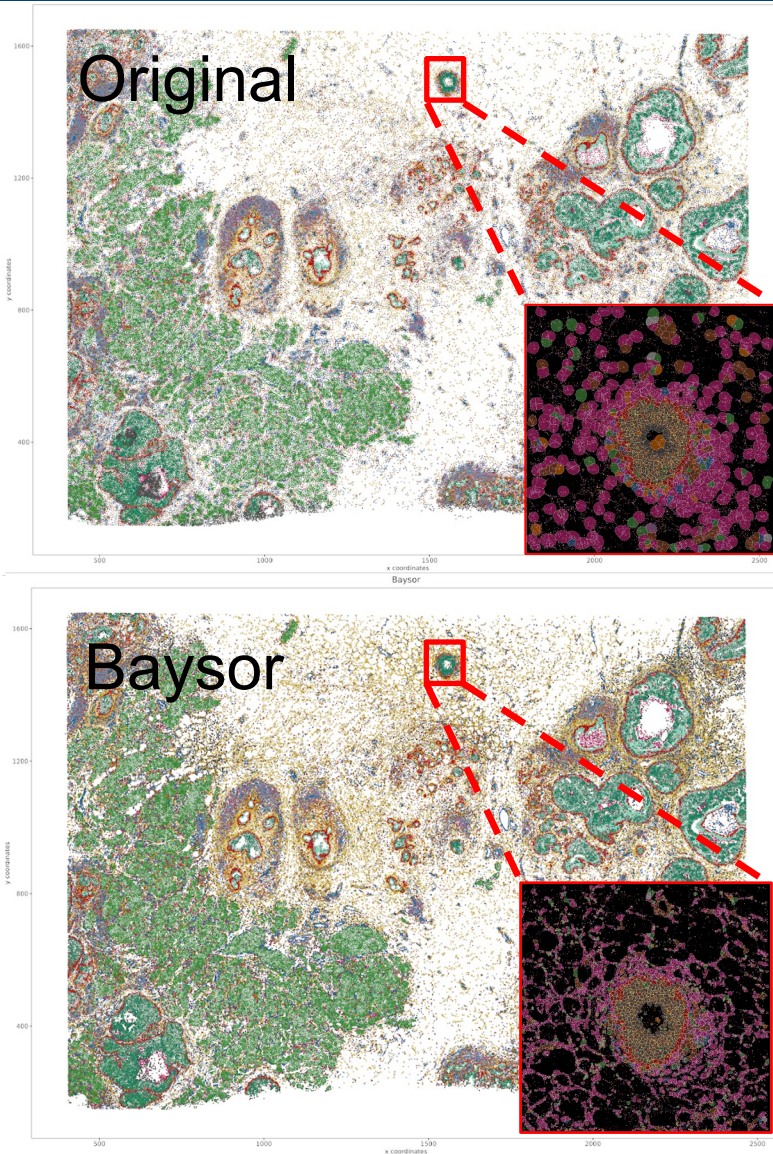
Co-registering and benchmarking cell segmentation effects



- B_Cells
- CD4+_T_Cells
- CD8+_T_Cells
- DCIS
- Dendritic_Cells
- Endothelial
- Invasive_Tumor
- Macrophage_M1
- Macrophage_M2
- Mast_Cells
- Myoepithelium_ACTA2
- Myoepithelium_KRT15
- Stromal
- Stromal_and_Tumor



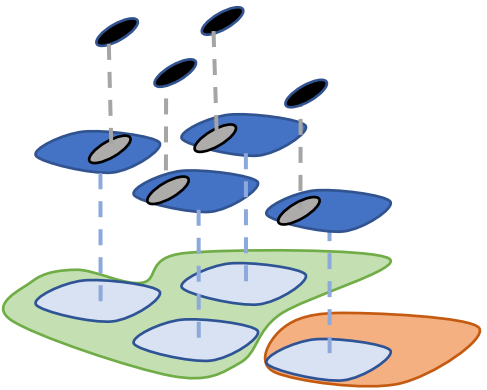
Co-registering and benchmarking cell segmentation effects



100% increase in stromal / Cancer-associated fibroblasts

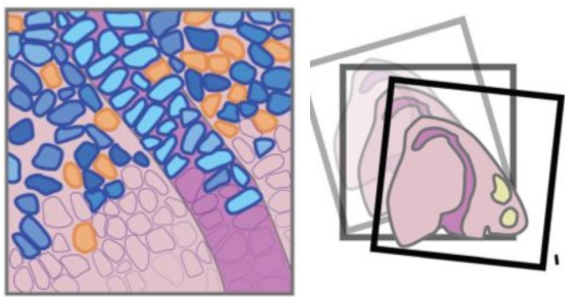
Tutorials & challenges:

Multi-scale



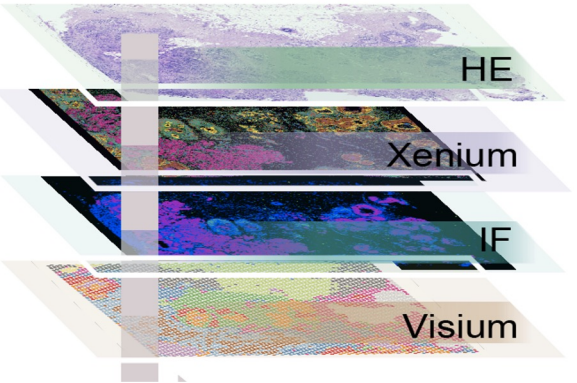
A diagram illustrating multi-scale analysis. At the bottom, a large green cell contains several smaller blue cells. Above it, several individual blue cells are shown at a higher magnification, with dashed lines indicating their correspondence to the cells in the larger cell below.

Registration & segmentation



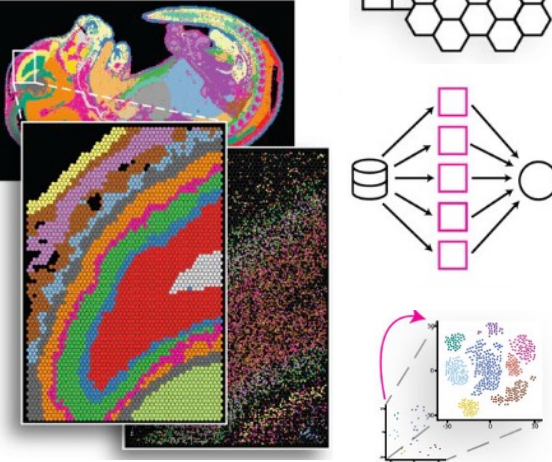
A diagram illustrating registration and segmentation. On the left, a histological image of tissue is shown with blue and orange regions. On the right, a corresponding anatomical map of a brain section is shown, with a black box indicating a region of interest that is being registered to the histological image.

Multi-modal



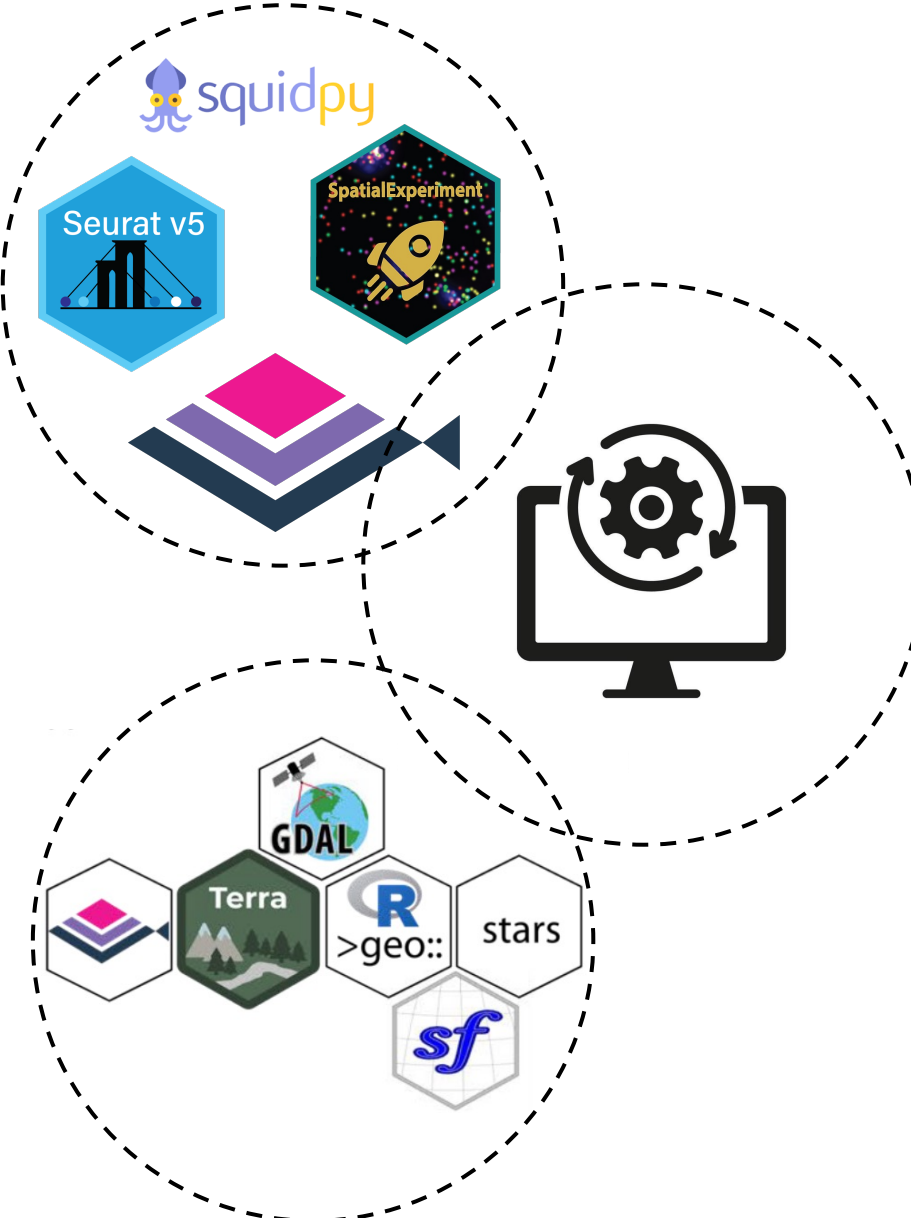
A diagram illustrating multi-modal data integration. It shows four stacked layers of data: HE (Histology), Xenium (Spatially Resolved Transcriptomics), IF (Immunofluorescence), and Visium (Spatially Resolved Transcriptomics). A vertical grey bar indicates a region of interest that is analyzed across all four modalities.

Scalability



A diagram illustrating scalability challenges and solutions. On the left, a large, colorful spatial transcriptomics image is shown. On the right, a grid of cells is shown, with a zoomed-in view of a single cell. Below the grid, a diagram shows a data flow from a database to a processing pipeline (represented by a vertical stack of boxes) and finally to a visualization of a cell cluster.

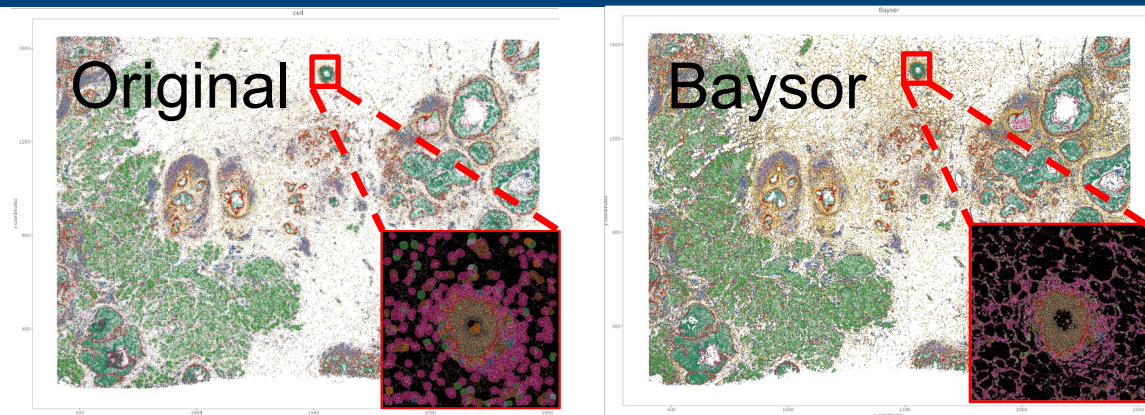
Community & tool building:



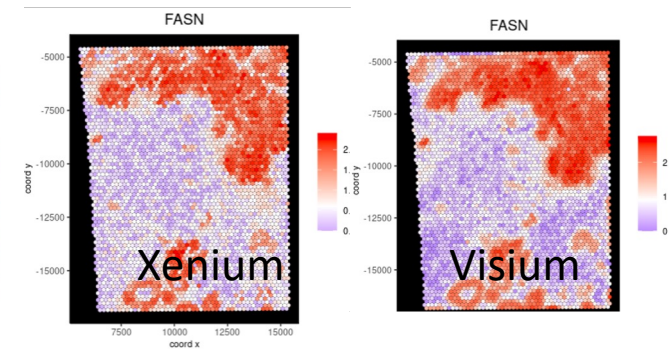
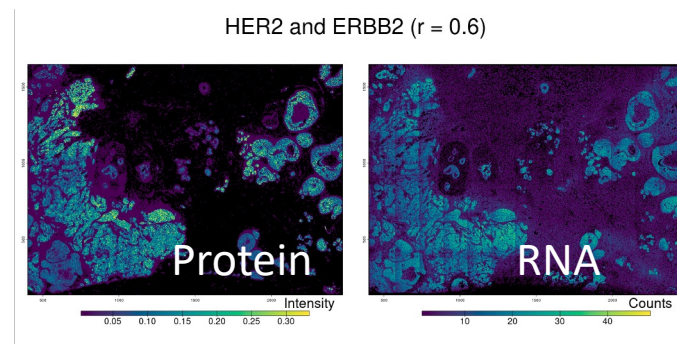
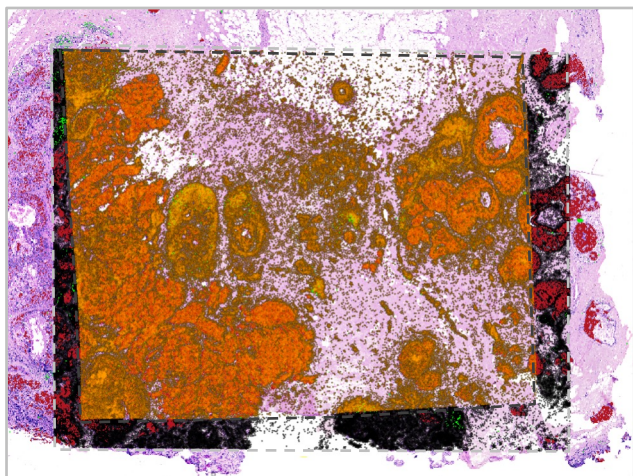
A diagram illustrating community and tool building. It features several interconnected circles and icons. The top circle contains logos for squidpy, Seurat v5, and SpatialExperiment. The bottom circle contains logos for GDAL, Terra, >geo::, stars, and sf. A central icon shows a computer monitor with a gear and a circular arrow, representing a workflow or tool. The circles are connected by dashed lines, indicating a network of tools and community members.

Co-registering and comparing different modalities

1. compare segmentation methods:



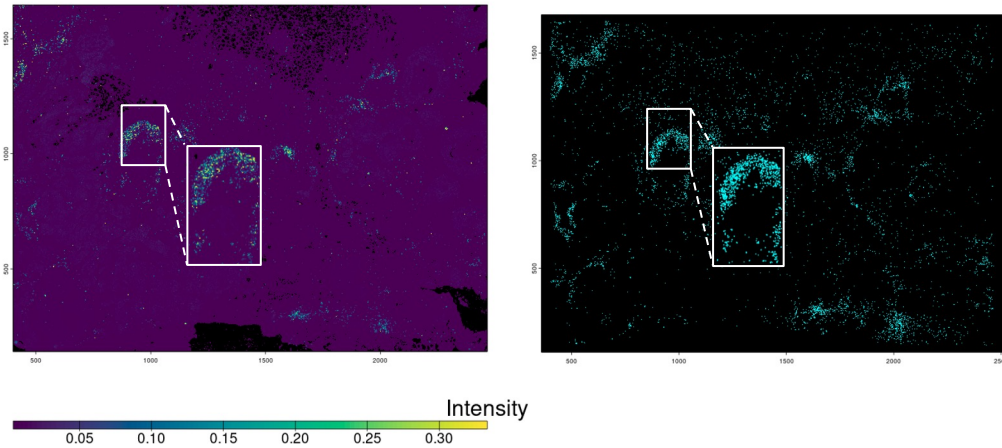
2. Compare modalities or technologies:



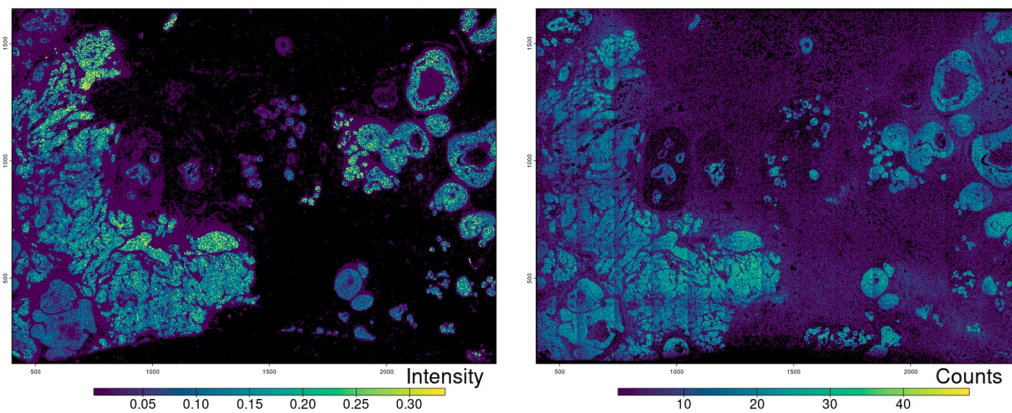
Co-registering and comparing different modalities

Protein vs RNA

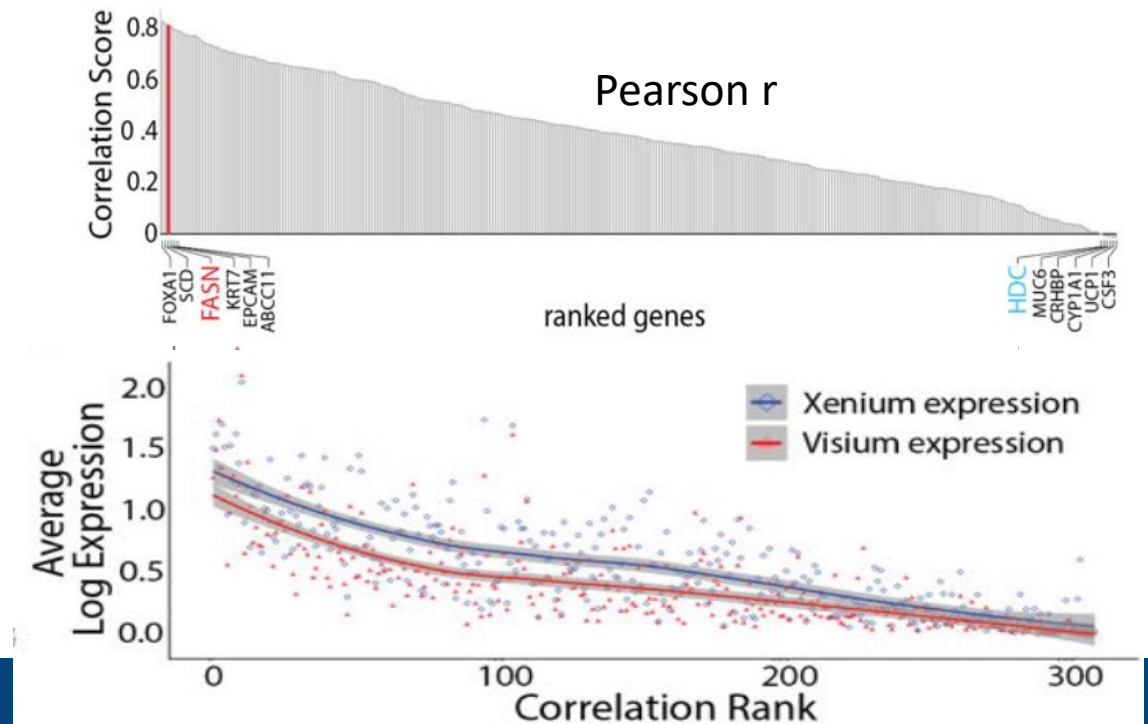
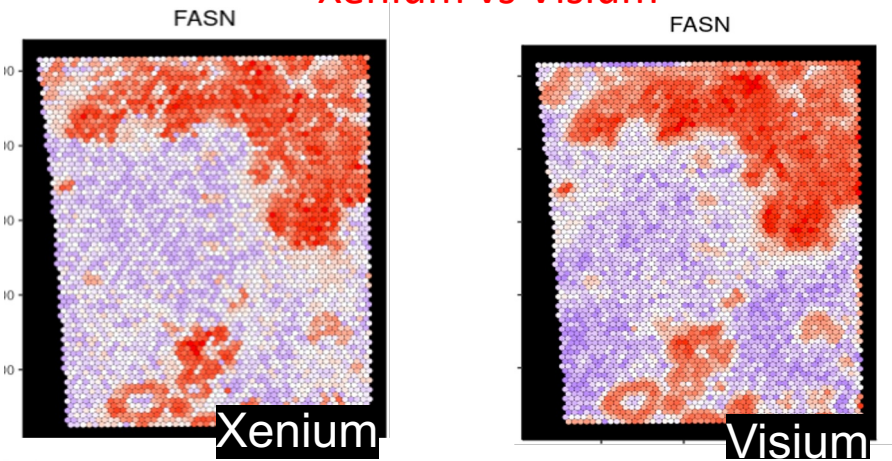
CD20 and MS4A1 ($r = 0.21$)



HER2 and ERBB2 ($r = 0.6$)

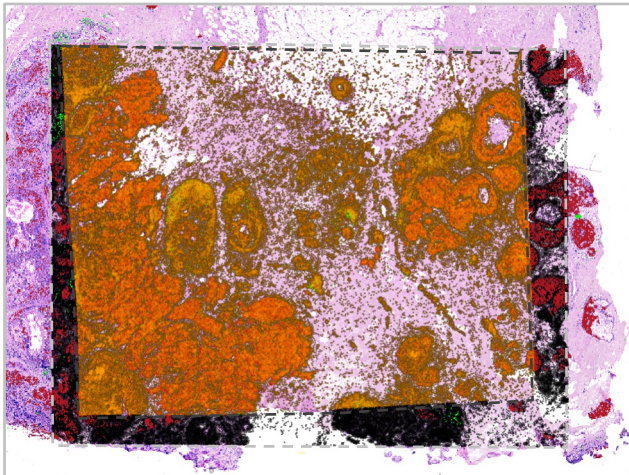
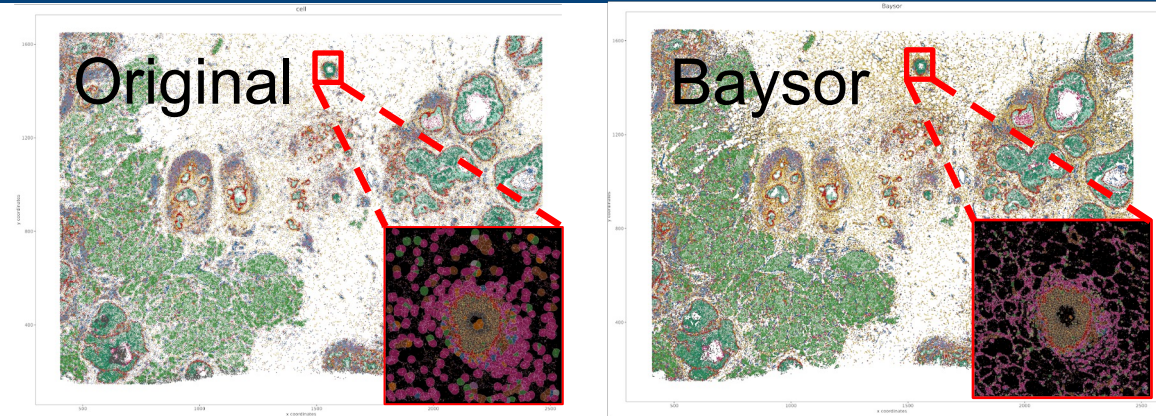


Xenium vs Visium

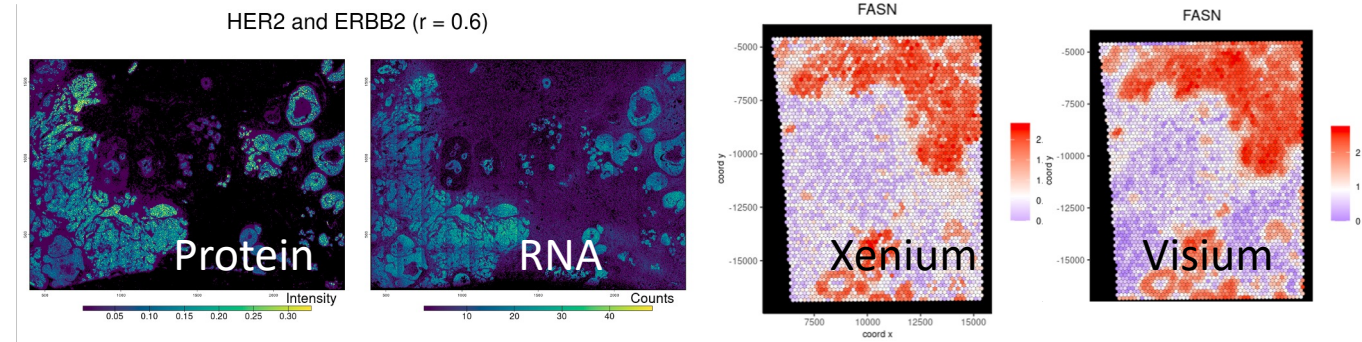


Co-registering and multi-modal data analysis

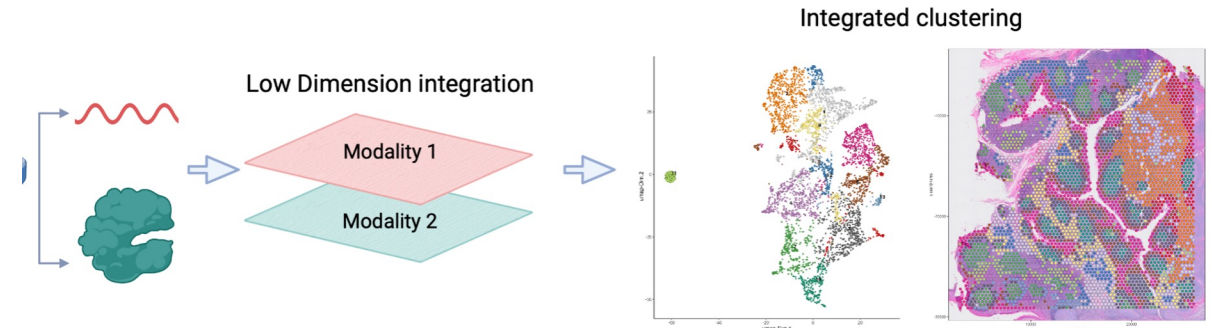
1. compare segmentation methods:



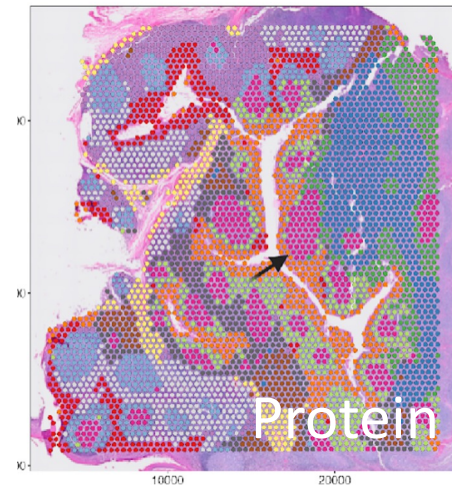
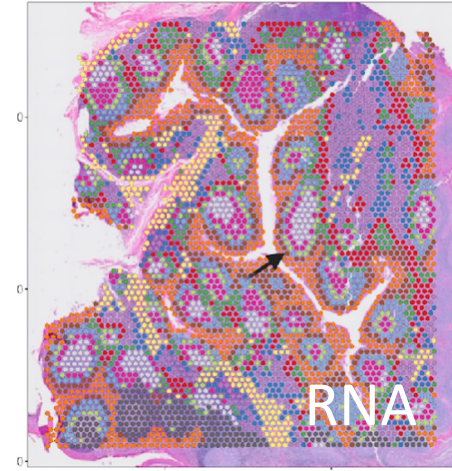
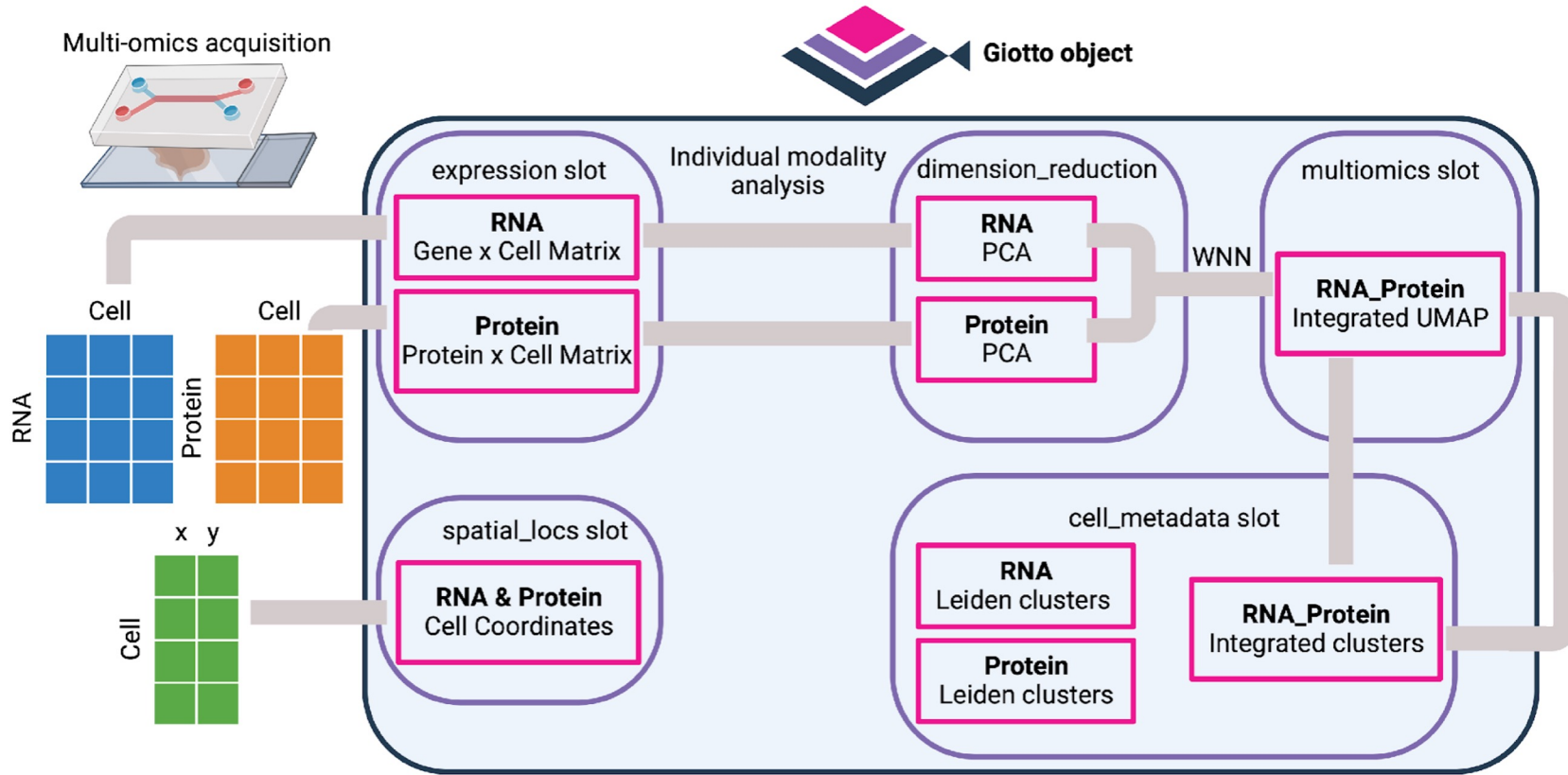
2. Compare modalities or technologies:



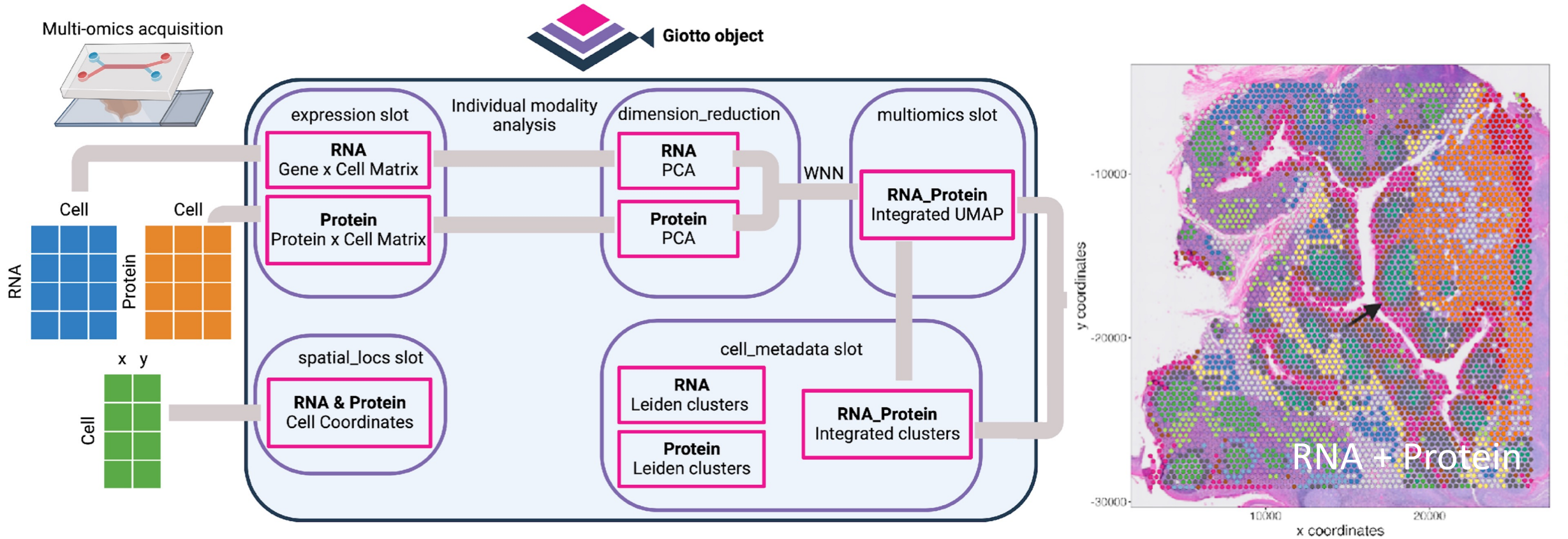
3. Joint-cluster:



Co-registering and multi-modal data analysis

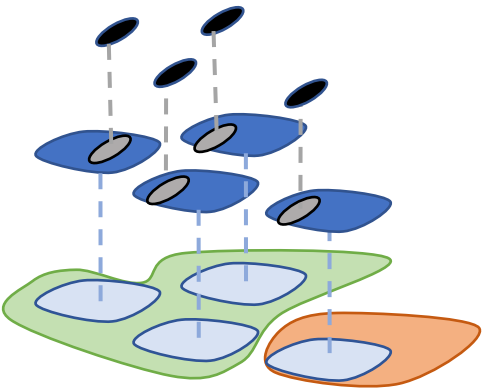


Co-registering and multi-modal data analysis



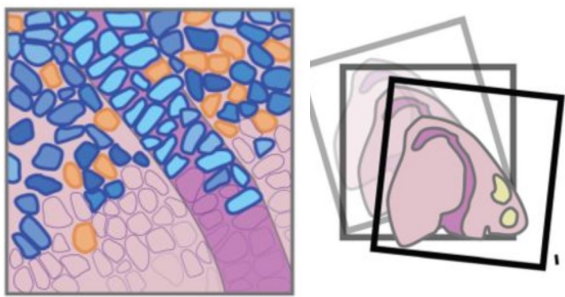
Tutorials & challenges:

Multi-scale



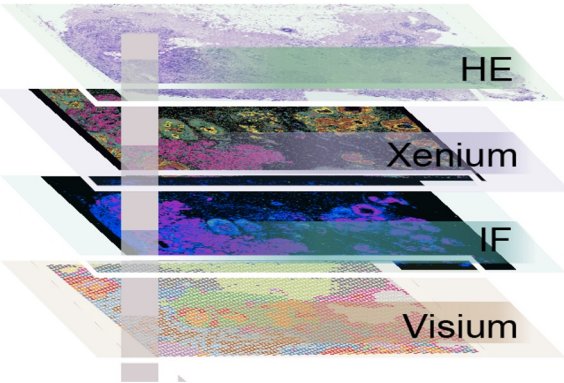
A diagram illustrating multi-scale analysis. At the bottom, a large green cell contains several smaller blue cells. Above it, several individual blue cells are shown at a higher magnification, with dashed lines indicating their correspondence to the cells in the larger cell below.

Registration & segmentation



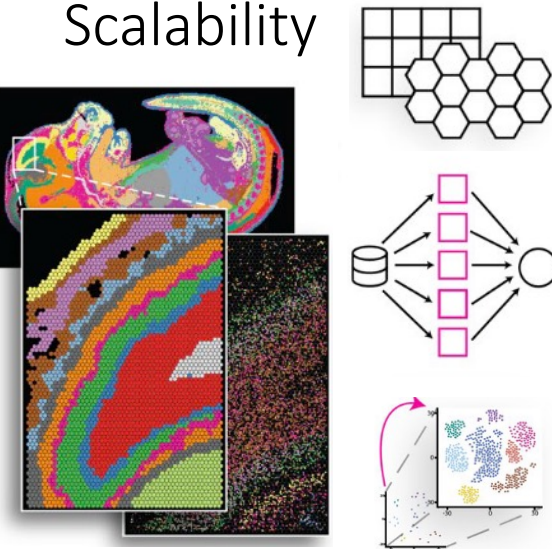
A diagram illustrating registration and segmentation. On the left, a histological image of tissue is shown with blue and orange regions. On the right, a corresponding anatomical map of a brain slice is shown, with a black box indicating a region of interest that is being registered to the histological image.

Multi-modal



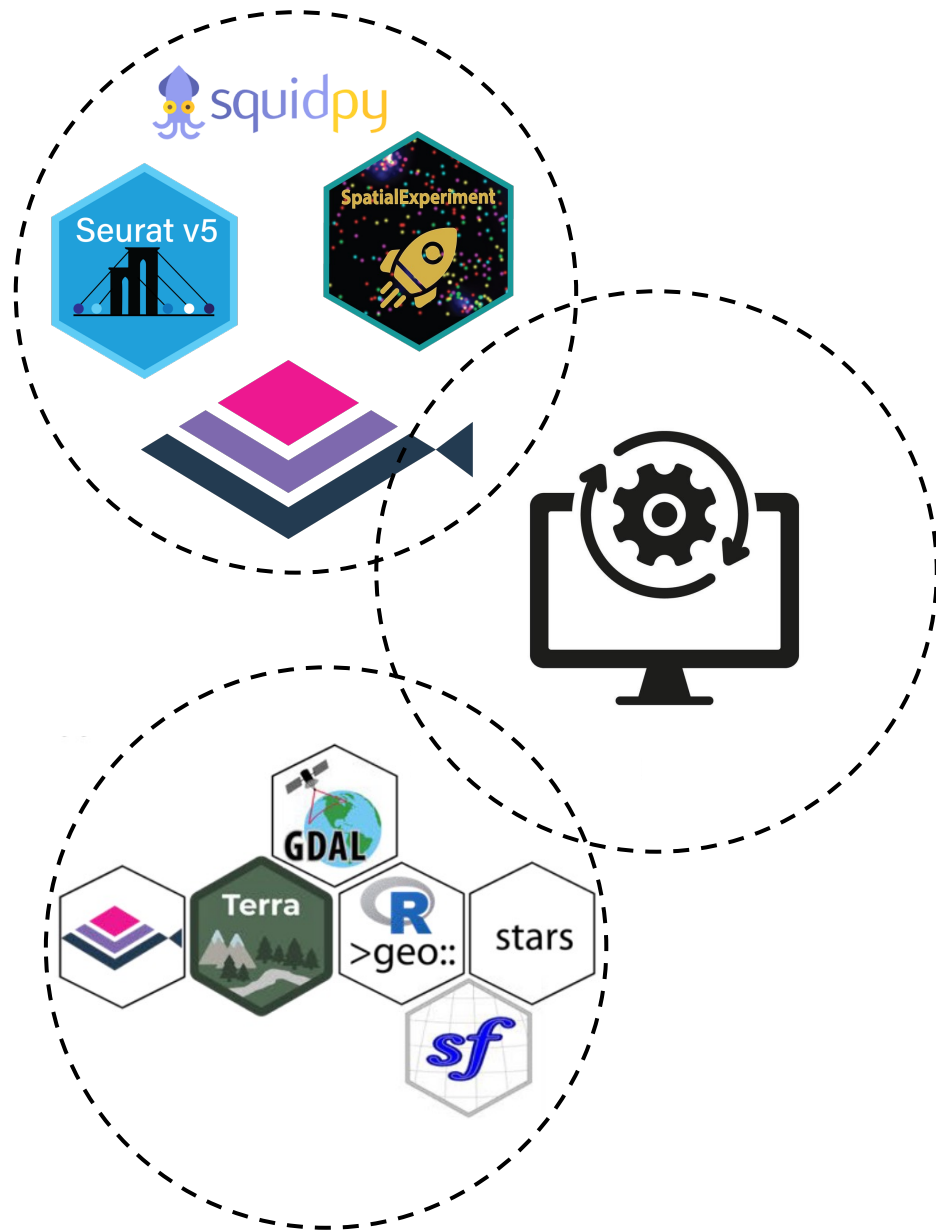
A diagram illustrating multi-modal data integration. It shows four stacked layers of data: HE (Histology), Xenium (Spatially Resolved Transcriptomics), IF (Immunofluorescence), and Visium (Spatially Resolved Transcriptomics). A vertical grey bar indicates a region of interest that is analyzed across all four modalities.

Scalability



A diagram illustrating scalability challenges and solutions. It shows a large, colorful histological image being processed into a grid of smaller tiles. To the right, a diagram shows a grid of cells being processed by a pipeline of four pink boxes, representing a scalable workflow. Below that, a diagram shows a large image being processed into a smaller, more manageable format.

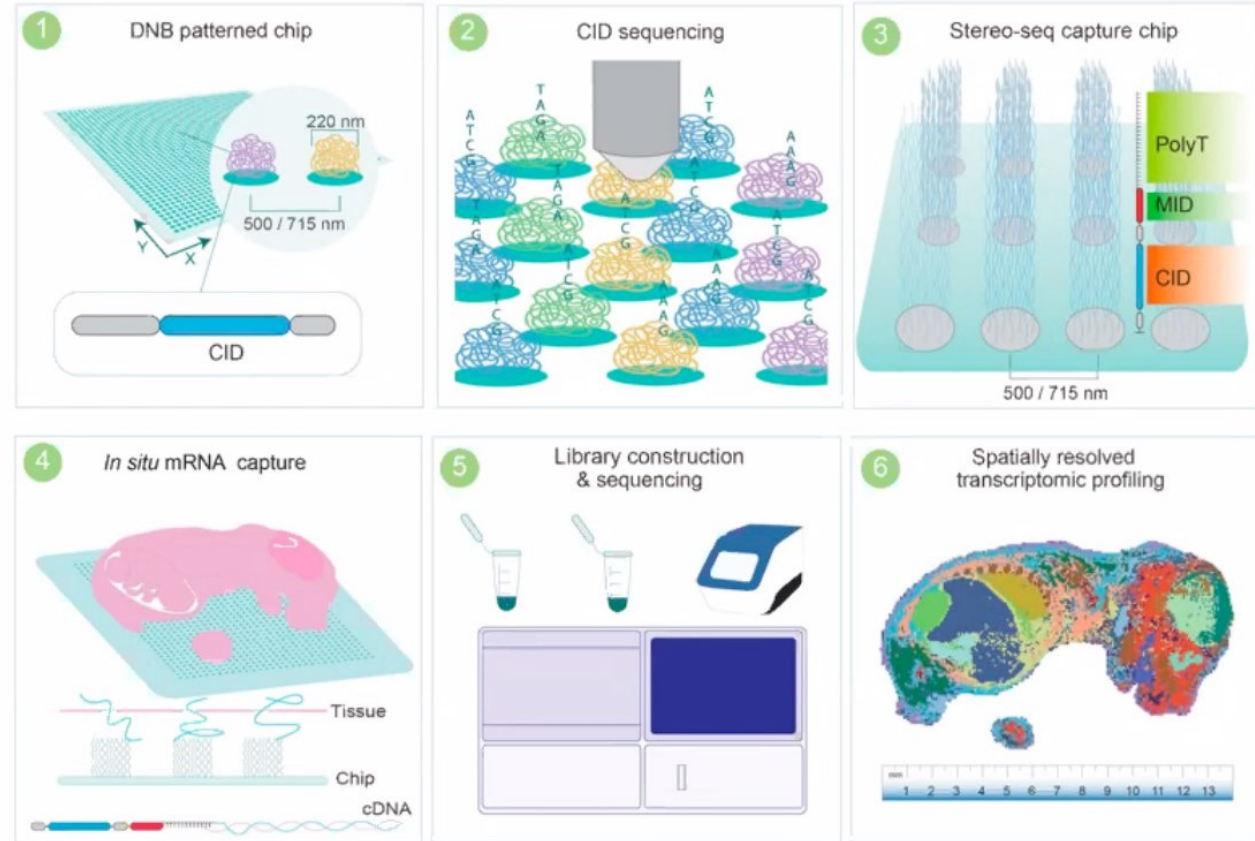
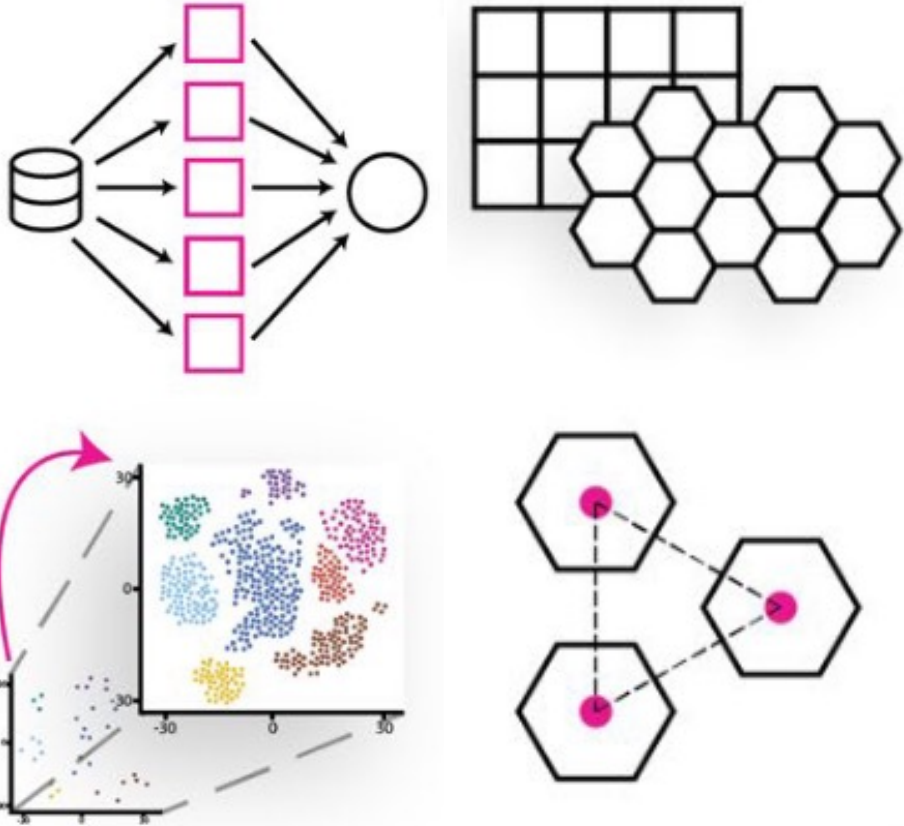
Community & tool building:



A diagram illustrating community and tool building. It features a central computer monitor icon with a gear and a circular arrow, representing a workflow or tool. Surrounding this are two large dashed circles. The top circle contains logos for squidpy, Seurat v5, and SpatialExperiment. The bottom circle contains logos for GDAL, Terra, >geo::, stars, and sf. A central stack of colored squares (pink, purple, blue) is also present.

Complex spatial data are **BIG** data – scalability solutions

Stereo-seq generates high-throughput high-resolution panoramic data

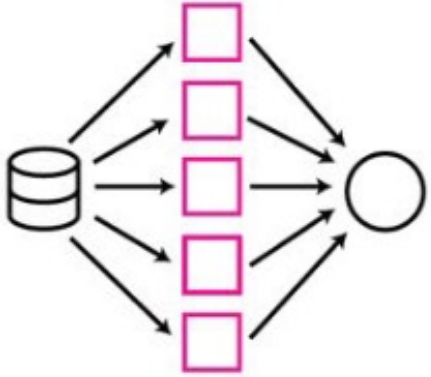


Chen et al., *BioRxiv*, 2021

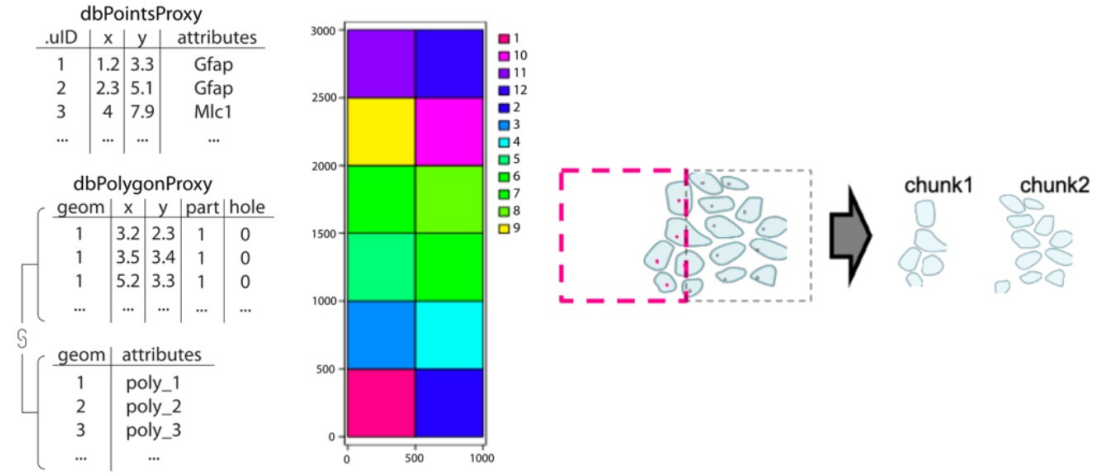
Complex spatial data are **BIG** data – scalability solutions

1. Code optimization

- **Bioc DelayedArray**
- **Bioc Future**

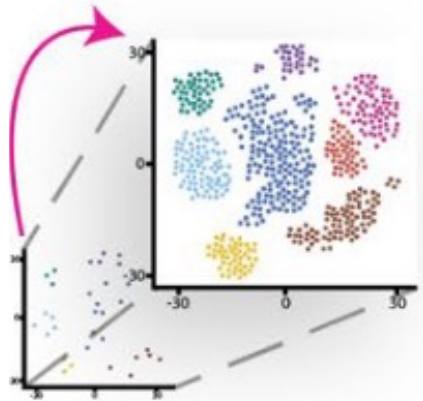


2. Spatial chunking

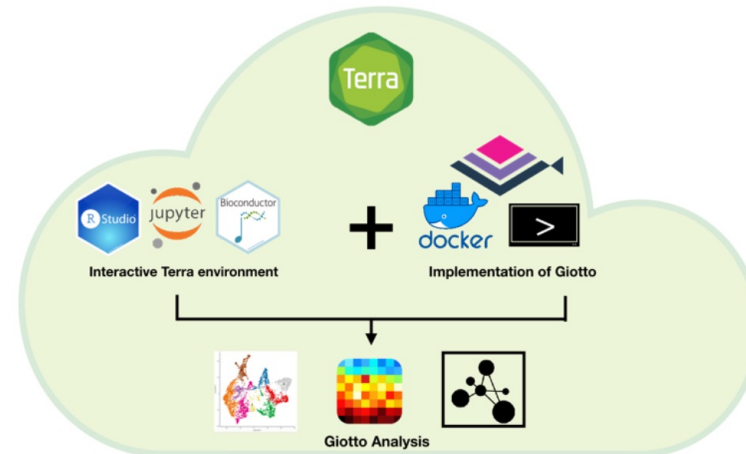


3. Data projections

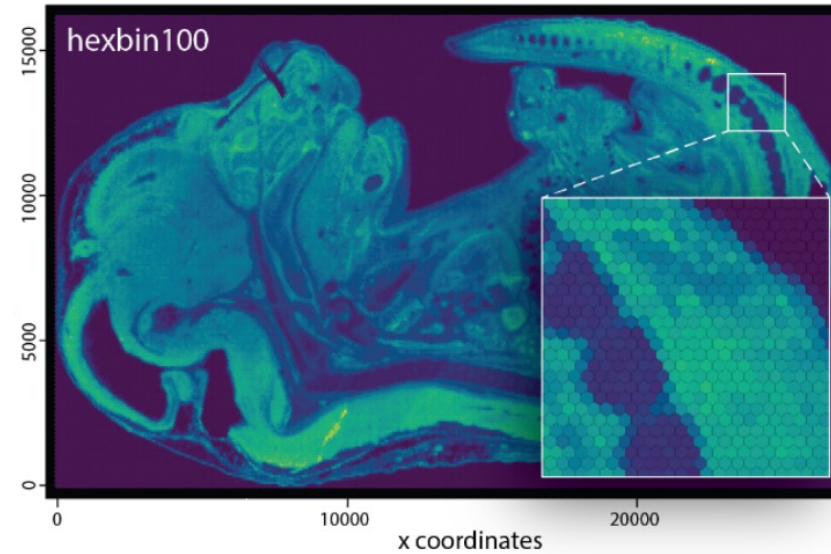
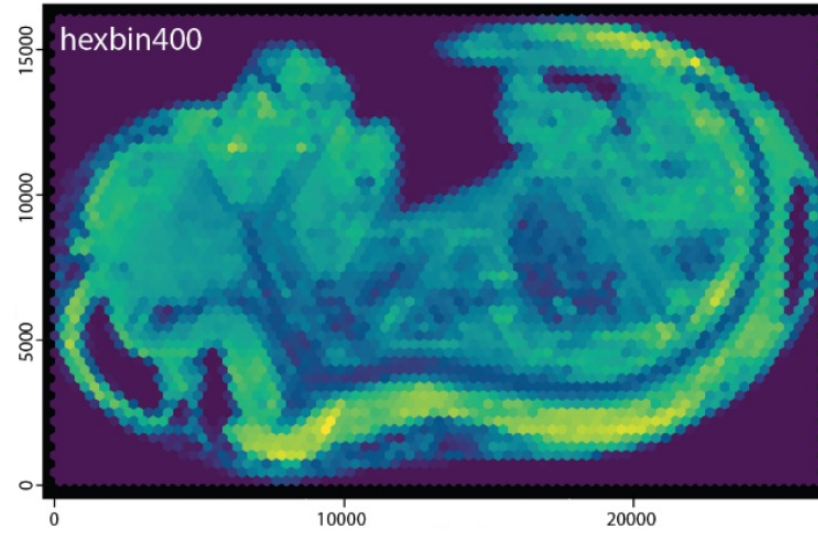
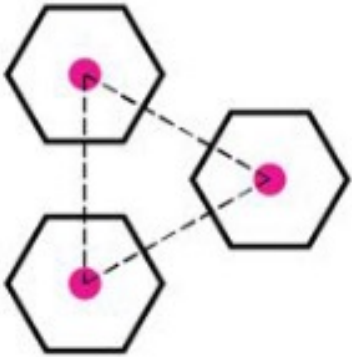
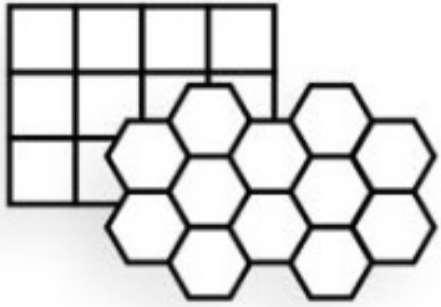
- **PCA**
- **UMAP**
- **Cluster annotations**



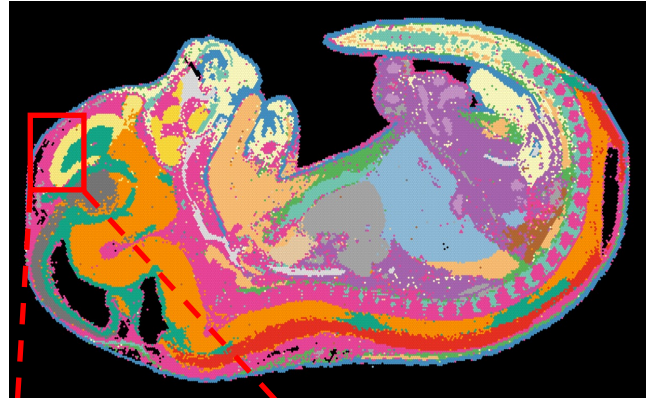
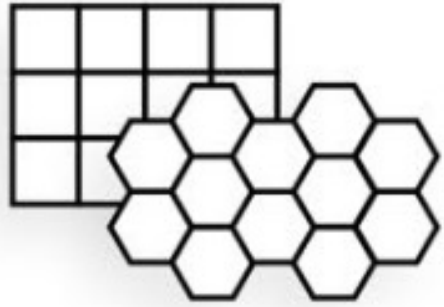
4. Infrastructure scaling



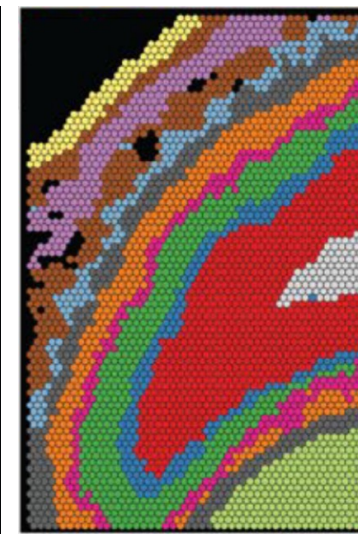
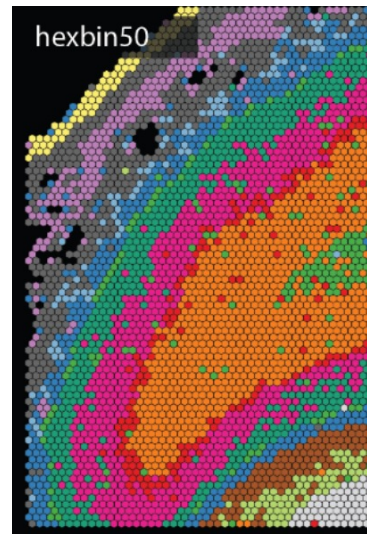
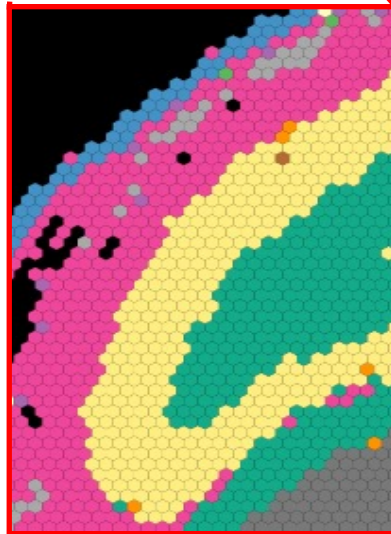
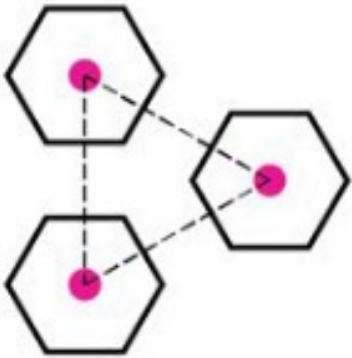
Complex spatial data are **BIG** data – flexible tiling



Complex spatial data are **BIG** data – additional tiling strategies



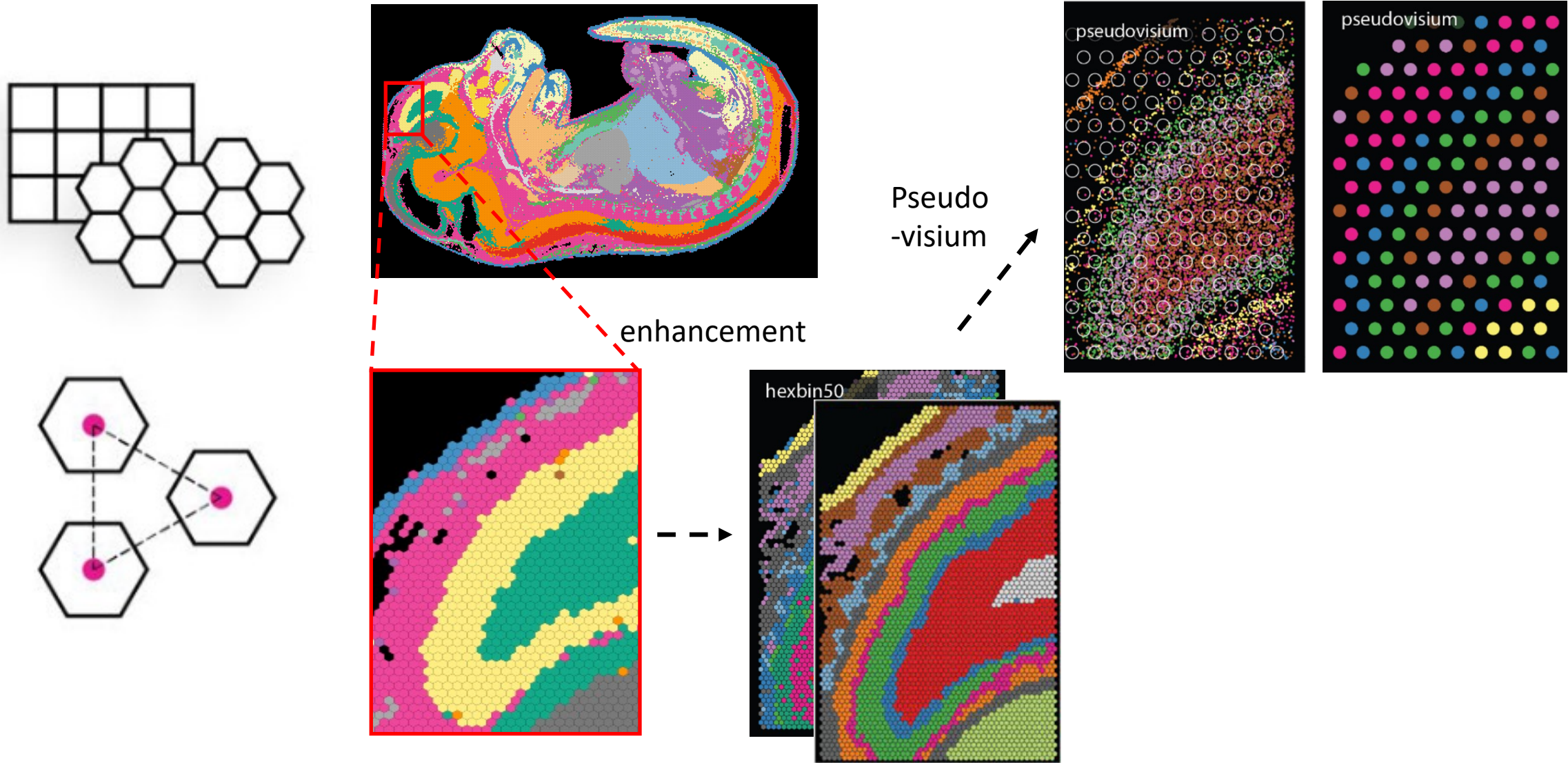
enhancement



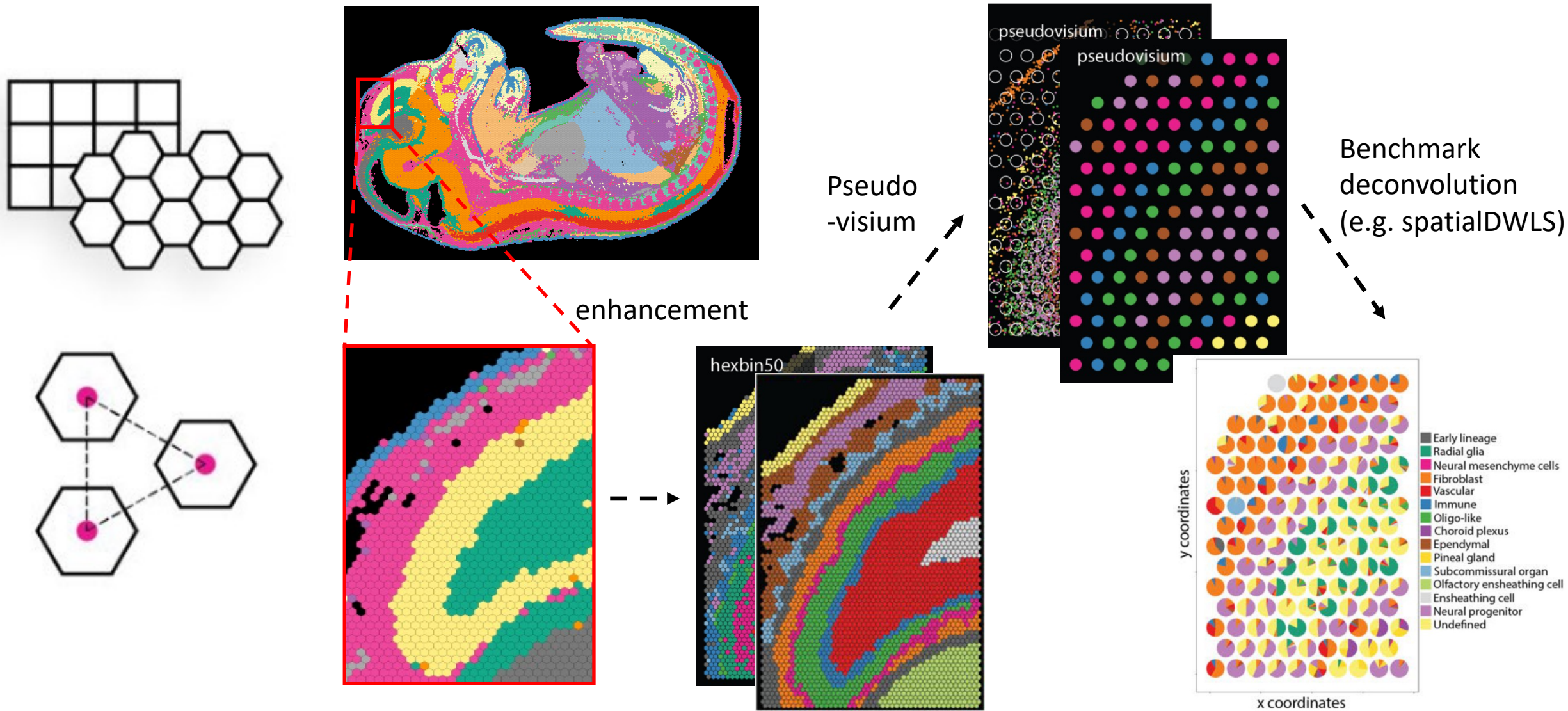
Alternative clustering strategies:

- Leiden / Louvain
- Niche composition
- Co-expression patterns
- HMRF
- ...

Complex spatial data are **BIG** data – additional tiling strategies

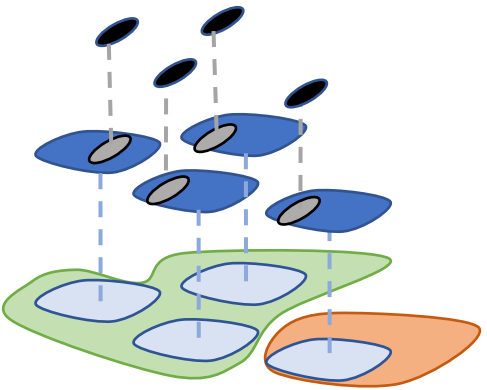


Complex spatial data are **BIG** data – additional tiling strategies



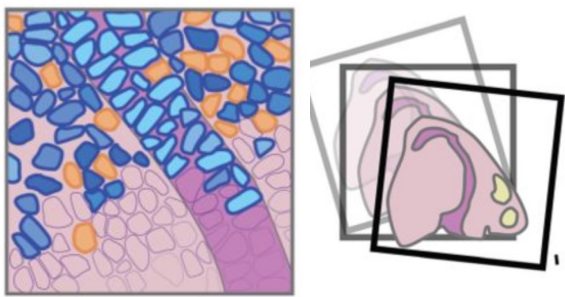
Tutorials & challenges:

Multi-scale



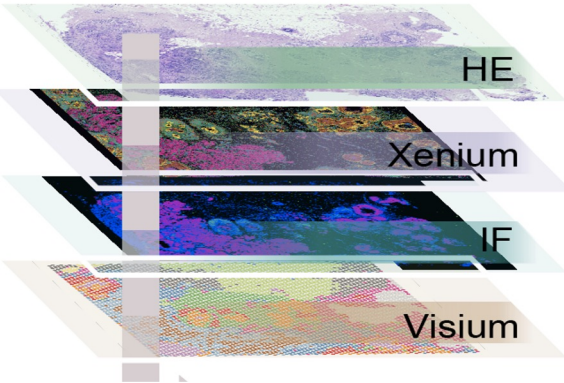
A diagram illustrating multi-scale analysis. At the bottom, a large green cell contains several smaller blue cells. Above it, several individual blue cells are shown at a higher magnification, with dashed lines indicating their correspondence to the cells in the larger cell below.

Registration & segmentation



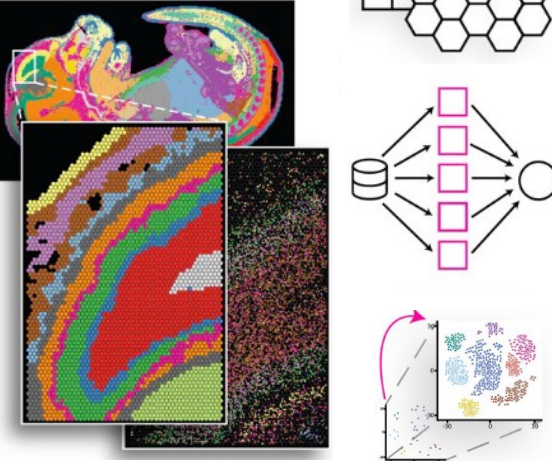
A diagram illustrating registration and segmentation. On the left is a histology slide with blue and orange cells. On the right is a brain slice with a yellow region highlighted. A black frame is shown overlapping the brain slice, representing the registration process.

Multi-modal



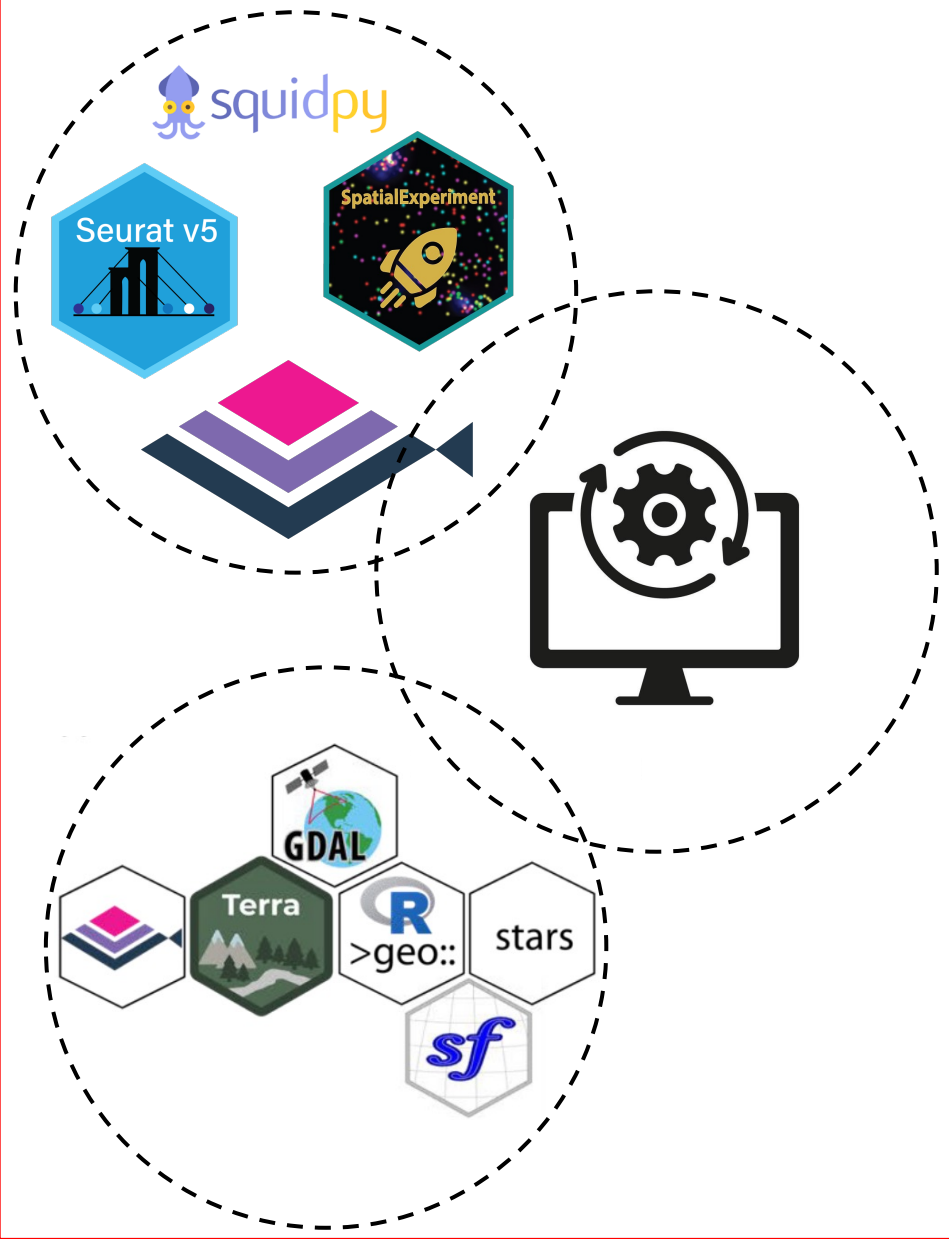
A diagram illustrating multi-modal data. It shows four layers of data: HE (Histology), Xenium (Spatially Resolved Transcriptomics), IF (Immunofluorescence), and Visium (Spatial Transcriptomics). Each layer is represented by a different color and texture, showing how they overlap and provide complementary information.

Scalability



A diagram illustrating scalability. It shows a grid of cells, a brain slice, and a data flow diagram. The data flow diagram consists of a central circle connected to a vertical stack of four squares, which are then connected to a larger circle on the right. Below this is a small map showing a spatial distribution of data points.

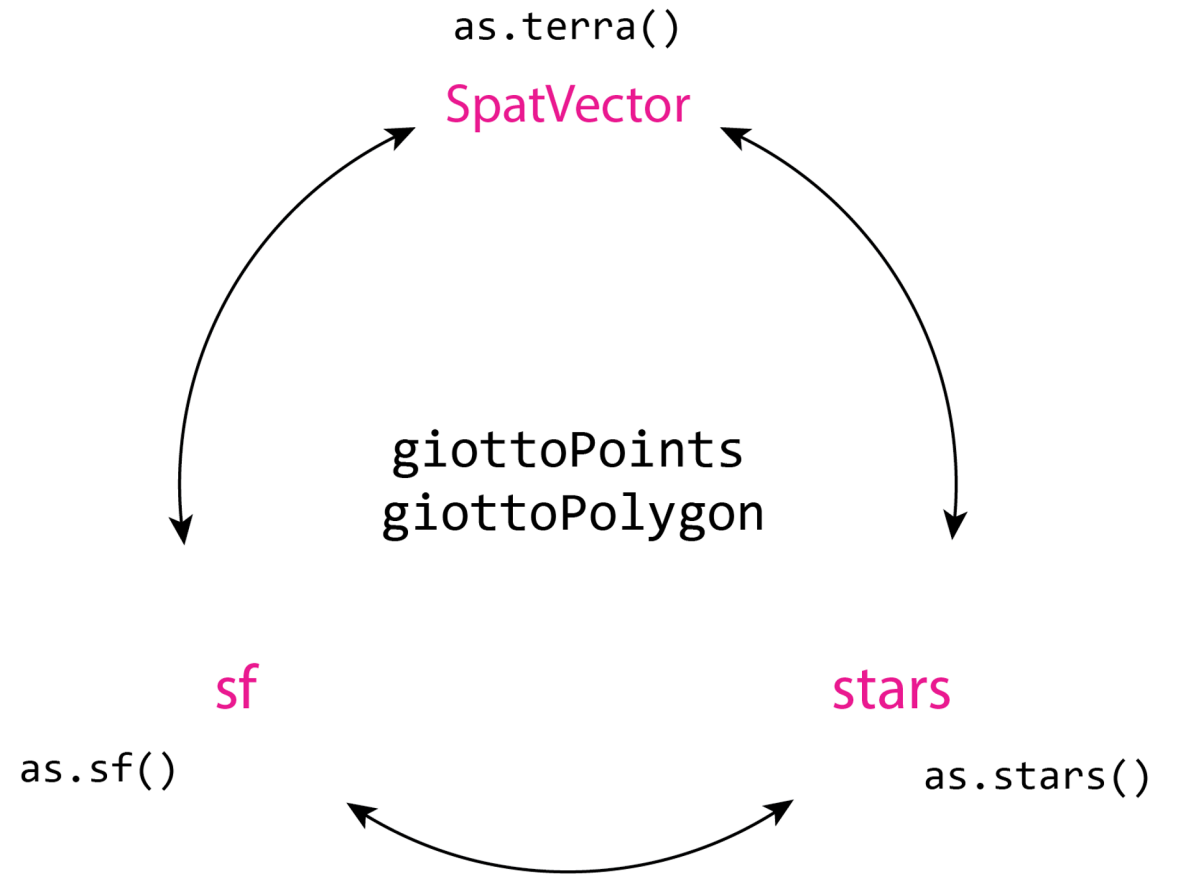
Community & tool building:



A diagram illustrating community and tool building. It features a central gear icon on a monitor, surrounded by various tools and frameworks. The tools include squidpy, Seurat v5, SpatialExperiment, GDAL, Terra, >geo::, stars, and sf. The diagram is enclosed in a red border.

Giotto Suite leverages decades of spatial (geo-)statistics work

R Spatial Ecosystem



Giotto Suite leverages decades of spatial (geo-)statistics work

R Spatial Ecosystem



Giotto Suite leverages decades of spatial (geo-)statistics work

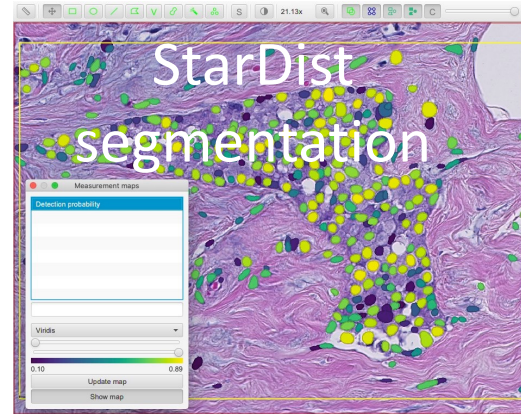
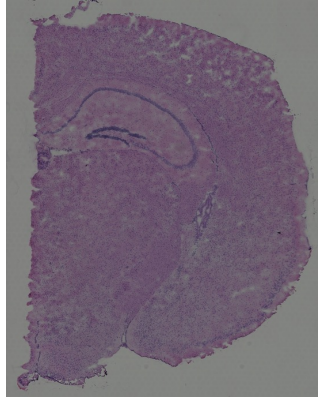
R Spatial Ecosystem



- Scale and distance
 - Introduction
 - Scale and resolution
 - Zonation
 - Distance
 - Distance matrix
 - Distance for longitude/latitude
 - Spatial influence
 - Adjacency
 - Two nearest neighbours
 - Weights matrix
 - Spatial influence for polygons
 - Raster based distance metrics
 - distance
 - cost distance
 - resistance distance
- Spatial autocorrelation
 - Introduction
 - Temporal autocorrelation
 - Spatial autocorrelation
 - Example data
 - Adjacent polygons
 - Compute Moran's I
- Interpolation
 - Introduction
 - Temperature in California
 - 9.2 NULL model
 - proximity polygons
 - Nearest neighbour interpolation
 - Inverse distance weighted
 - California Air Pollution data
 - Data preparation
 - Fit a variogram
 - Ordinary kriging
 - Compare with other methods
 - Cross-validation
 - Spatial distribution models
 - Data
 - Observations
 - Predictor variables
 - Background data
 - East vs West
 - Fit a model
 - CART
 - Random Forest
- Predict
 - Regression
 - Classification
- Extrapolation
- Climate change
- Further reading
- Local regression
 - California precipitation
 - California House Price Data
 - Summarize
 - Regression
 - Geographically Weighted Regression
 - By county
 - By grid cell
 - spgwr package
- Spatial regression models
 - Introduction
 - Reading & aggregating data
 - Get the data
 - Basic OLS model
 - Spatial lag model
 - Spatial error model
 - Questions

Visium super-enhancement strategy

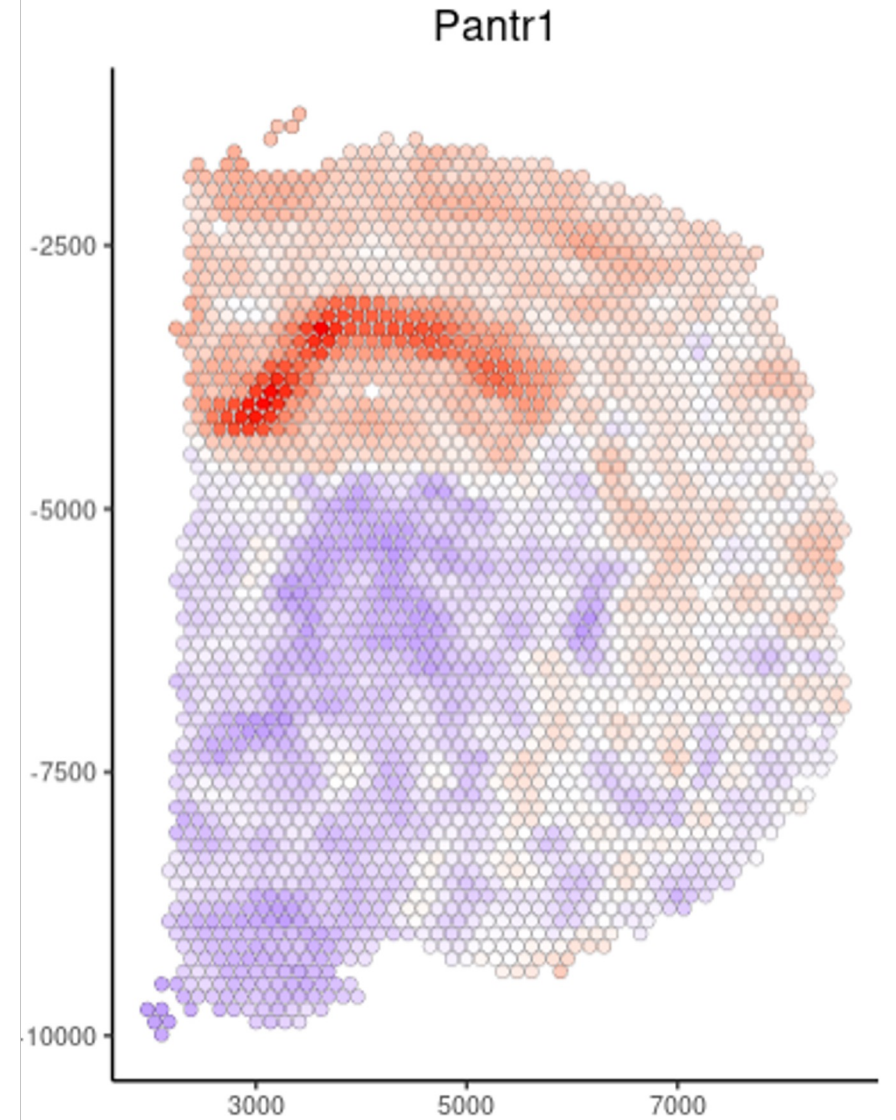
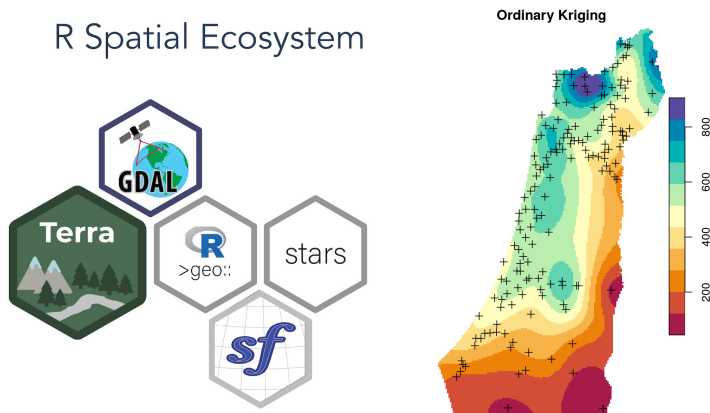
H&E single-cell segmentation



Giotto Suite

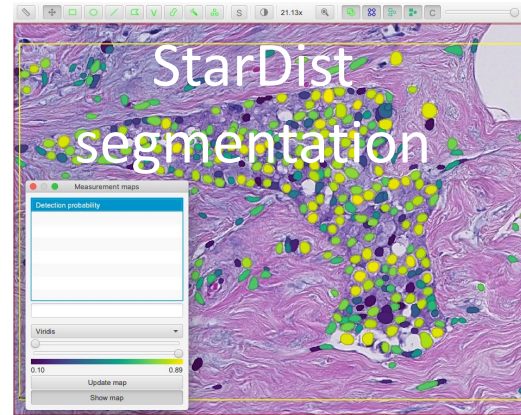
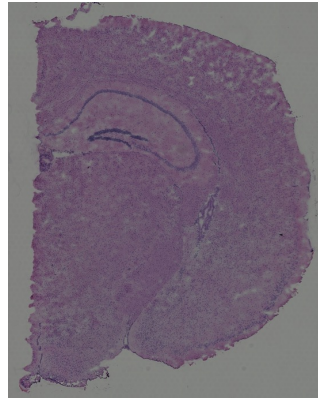


Spatial interpolation : kriging



Visium super-enhancement strategy

H&E single-cell segmentation



Giotto Suite

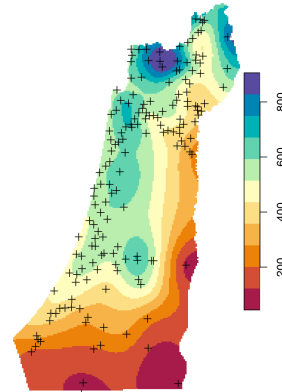
Spatial interpolation : kriging



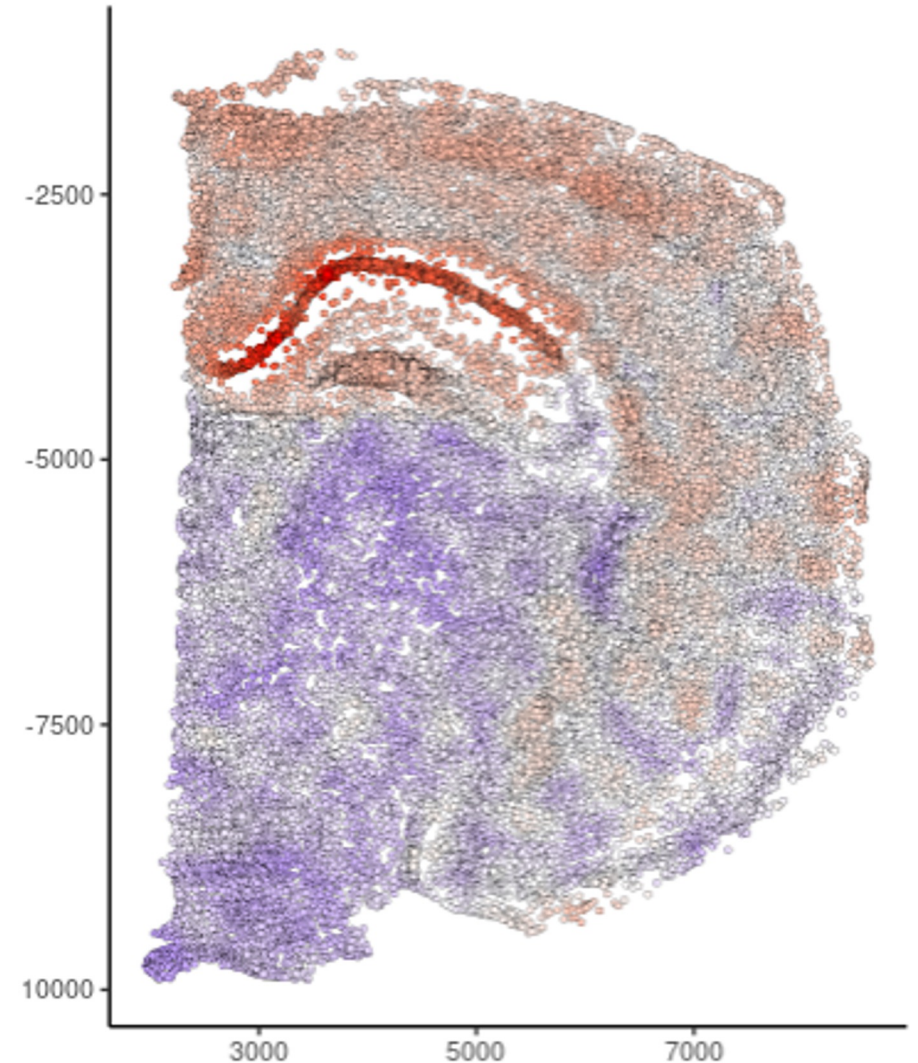
R Spatial Ecosystem



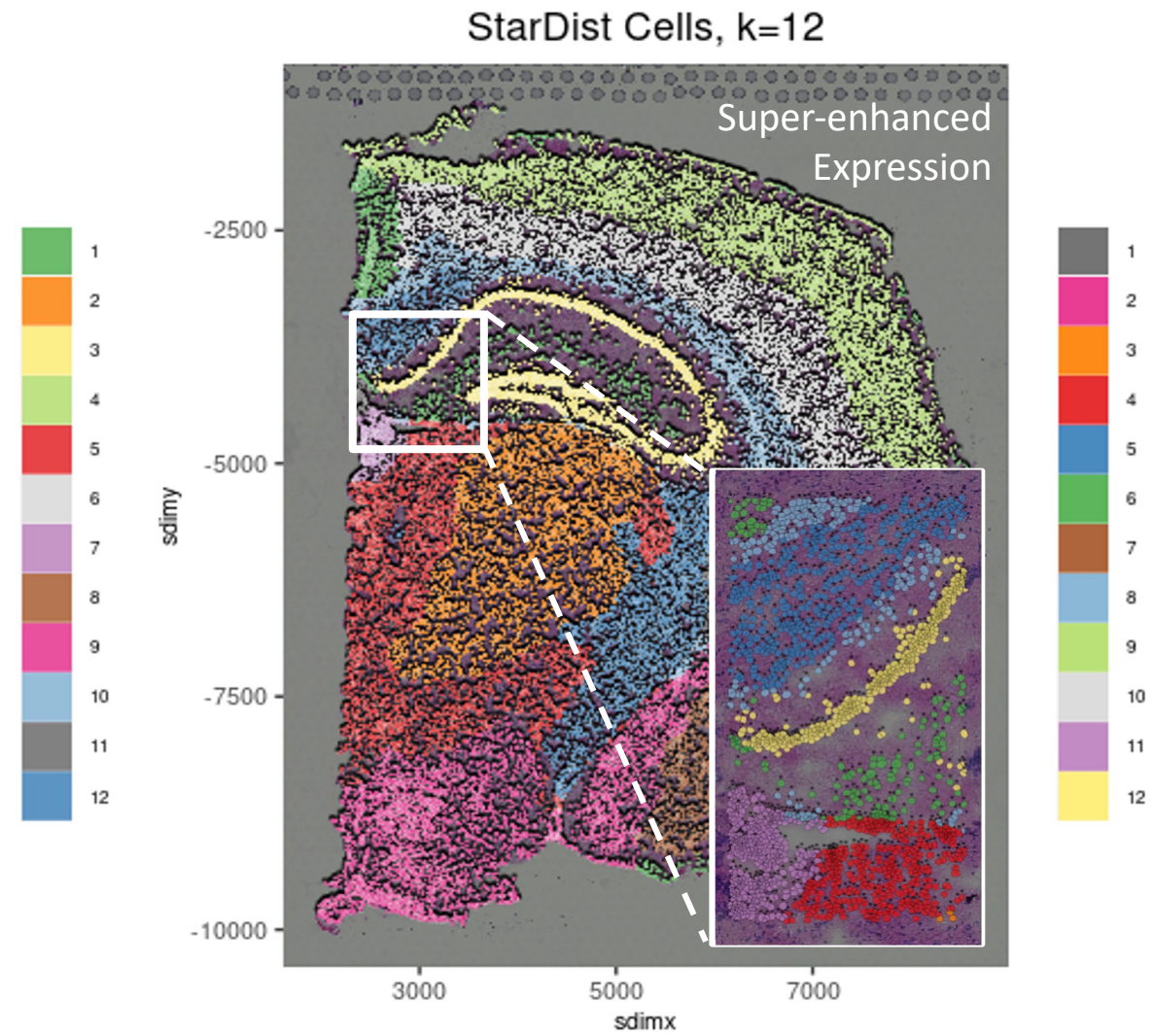
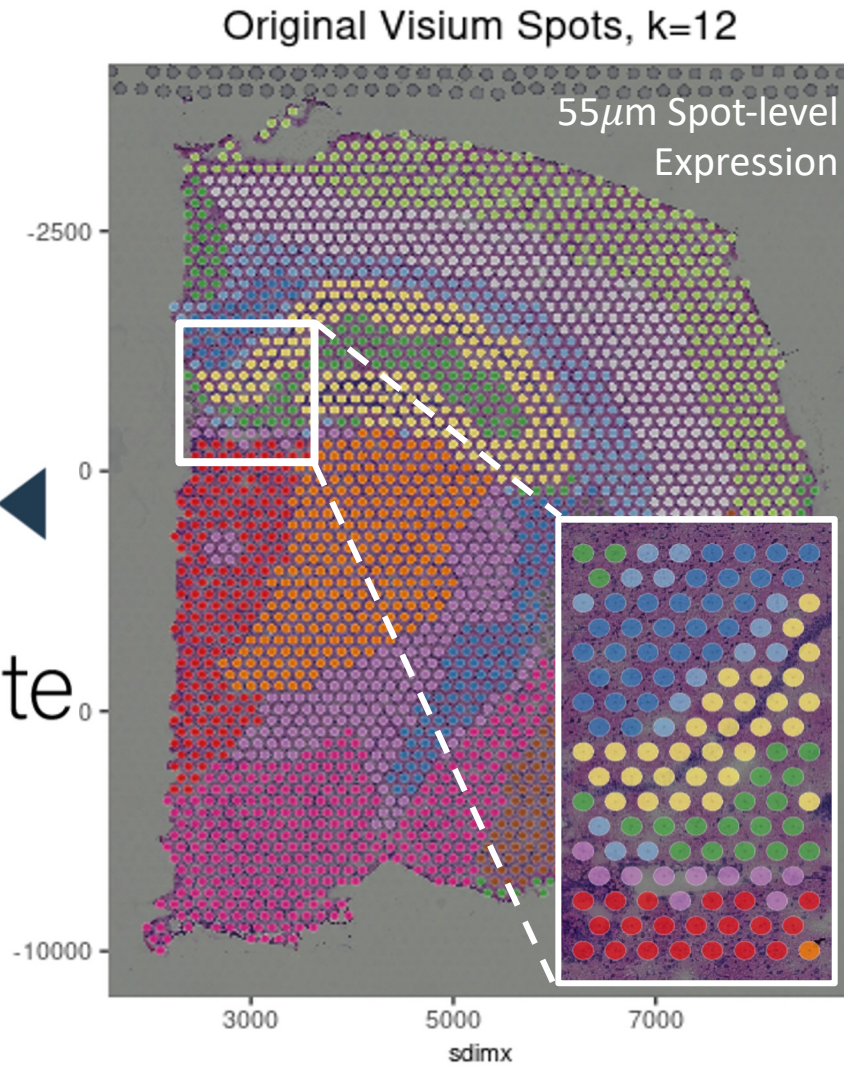
Ordinary Kriging



Pantr1



Visium super-enhancement strategy





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Giotto Suite: a multi-scale and technology-agnostic spatial multi-omics analysis ecosystem

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Giotto Suite



Giotto Suite is a major upgrade to the Giotto package that provides tools to process, analyze and visualize **spatial multi-omics data at all scales and multiple resolutions**. The underlying framework is generalizable to virtually all current and emerging spatial technologies. Our Giotto Suite prototype pipeline is generally applicable on various different datasets, such as those created by state-of-the-art spatial technologies, including *in situ* hybridization (seqFISH+, merFISH, osmFISH, CosMx), sequencing (Slide-seq, Visium, STARmap, Seq-Scope, Stereo-Seq) and imaging-based multiplexing/proteomics (CyCIF, MIBI, CODEX). These technologies differ in terms of resolution (subcellular, single cell or multiple cells), spatial dimension (2D vs 3D), molecular modality (protein, RNA, DNA, ...), and throughput (number of cells and analytes).

Installation

To install Giotto suite use `devtools::install_github("drieslab/Giotto")`.

Visit the Giotto [Discussions](#) page for more information.

Website Update!

With Giotto version 4.0, we updated the website at <http://giottosuite.com>, you can still find the previous website at <https://giottosuite.readthedocs.io/en/latest/>

Website description

- **Get started:** Here you can find more advanced information about the Giotto object, Giotto ecosystem, Giotto configuration, and installation FAQs.
- **Documentation:** Here you will find all Giotto functions grouped by their purpose (Helpers, Getters & Setters, Visualization, ...)
- **Examples:** Here you can find end-to-end examples for different technologies and datasets.
- **Tutorials:** Here you can find various tutorials on working with Giotto (analysis, visualizations, working on the cloud, ...)
- **News:** Here you can find the changelog for every Giotto release and video recordings from previous presentations.

Links

[Browse source code](#)

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GPL (>= 3)

Community

[Contributing guide](#)

[Code of conduct](#)

Citation

[Citing Giotto](#)

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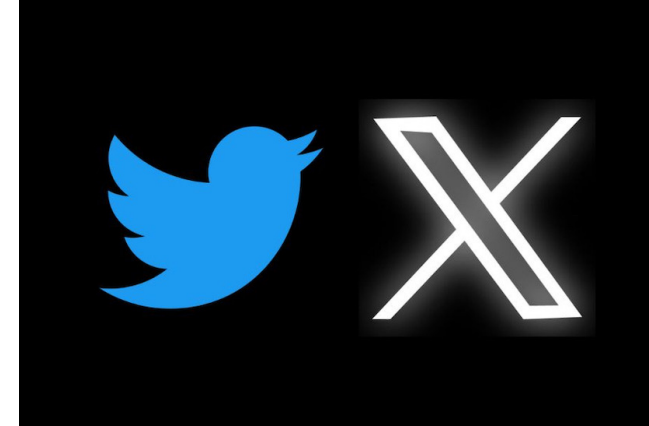


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TESTER

Interested to:

- Contribute to Giotto?
- Add your tool to Giotto?
- Collaborate?

Reach out to rdries@bu.edu



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